



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.



Forecasting on Covid-19 infection waves using a rough set filter driven moving average models



Saurabh Ranjan Srivastava*, Yogesh Kumar Meena, Girdhari Singh

Malviya National Institute of Technology, Jaipur, India

ARTICLE INFO

Article history:

Received 22 February 2022

Received in revised form 9 October 2022

Accepted 17 October 2022

Available online 2 November 2022

Keywords:

Covid-19
Moving average
Rough set
Pandemic
Forecast

ABSTRACT

The pandemic outbreak of severe acute respiratory syndrome caused by the Coronavirus 2 disease in 2019, also known as SARS-COV-2 and COVID-19, has claimed over 5.6 million lives till now. The highly infectious nature of the Covid-19 virus has resulted into multiple massive upsurges in counts of new infections termed as 'waves.' These waves consist of numerous rising and falling counts of Covid-19 infection cases with changing dates that confuse analysts and researchers. Due to this confusion, the detection of emergence or drop of Covid waves is currently a subject of intensive research. Hence, we propose an algorithmic framework to forecast the upcoming details of Covid-19 infection waves for a region. The framework consists of a displaced double moving average (δ DMA) algorithm for forecasting the start, rise, fall, and end of a Covid-19 wave. The forecast is generated by detection of potential dates with specific counts called 'markers.' This detection of markers is guided by decision rules generated through rough set theory. We also propose a novel 'corrected moving average' (χ SMA) technique to forecast the upcoming count of new infections in a region. We implement our proposed framework on a database of Covid-19 infection specifics fetched from 12 countries, namely: Argentina, Colombia, New Zealand, Australia, Cuba, Jamaica, Belgium, Croatia, Libya, Kenya, Iran, and Myanmar. The database consists of day-wise time series of new and total infection counts from the date of first case till 31st January 2022 in each of the countries mentioned above. The δ DMA algorithm outperforms other baseline techniques in forecasting the rise and fall of Covid-19 waves with a forecast precision of 94.08%. The χ SMA algorithm also surpasses its counterparts in predicting the counts of new Covid-19 infections for the next day with the least mean absolute percentage error (MAPE) of 36.65%. Our proposed framework can be deployed to forecast the upcoming trends and counts of new Covid-19 infection cases under a minimum observation window of 7 days with high accuracy. With no perceptible impact of countermeasures on the pandemic until now, these forecasts will prove supportive to the administration and medical bodies in scaling and allotment of medical infrastructure and healthcare facilities.

© 2022 Elsevier B.V. All rights reserved.

1. Introduction

Will there be a next Covid wave? This question has been haunting human civilization since December 2019, when the Coronavirus disease emerged in the Hubei central province of China [1]. By the end of January 2020, the World Health Organization (WHO) declared Covid-19 a Public Health Emergency of International Concern (PHEIC) (Fig. 1). Since then, Covid-19 has evolved as a severe global pandemic that has instigated unprecedented havoc around the globe [2]. In the current state, the highly

contagious Covid-19 virus attacks the human respiratory system causing severe health issues and even death.

To date, the changing counts of Covid-19 infections in the population of every country are being regularly recorded. Several variants [3] of the Coronavirus have instigated numerous spikes and drops in these infection counts for multiple times in various regions of the world. At times, these spikes and drops together compose patterns of extreme upsurges and downturns for a noticeable period causing severe damage to lives and resources. Such patterns of infection counts and their behaviors have been termed as waves of the Covid-19 pandemic [4]. However, the spikes and drops are regularly witnessed phenomena in the recorded infection counts during waves as well as moderate periods. Therefore, distinguishing a temporary spike or a group of spikes in infection counts from an upcoming wave is a challenge. Ignorance of an approaching infection wave as a transitory spike

* Correspondence to: Department of Computer Science & Engineering, Malviya National Institute of Technology, Jaipur, JLN Marg, Jaipur 302017, Rajasthan, India.

E-mail addresses: saurabhranjanjansrivastava@gmail.com (S.R. Srivastava), ymeena.cse@mnit.ac.in (Y.K. Meena), gsingh.cse@mnit.ac.in (G. Singh).

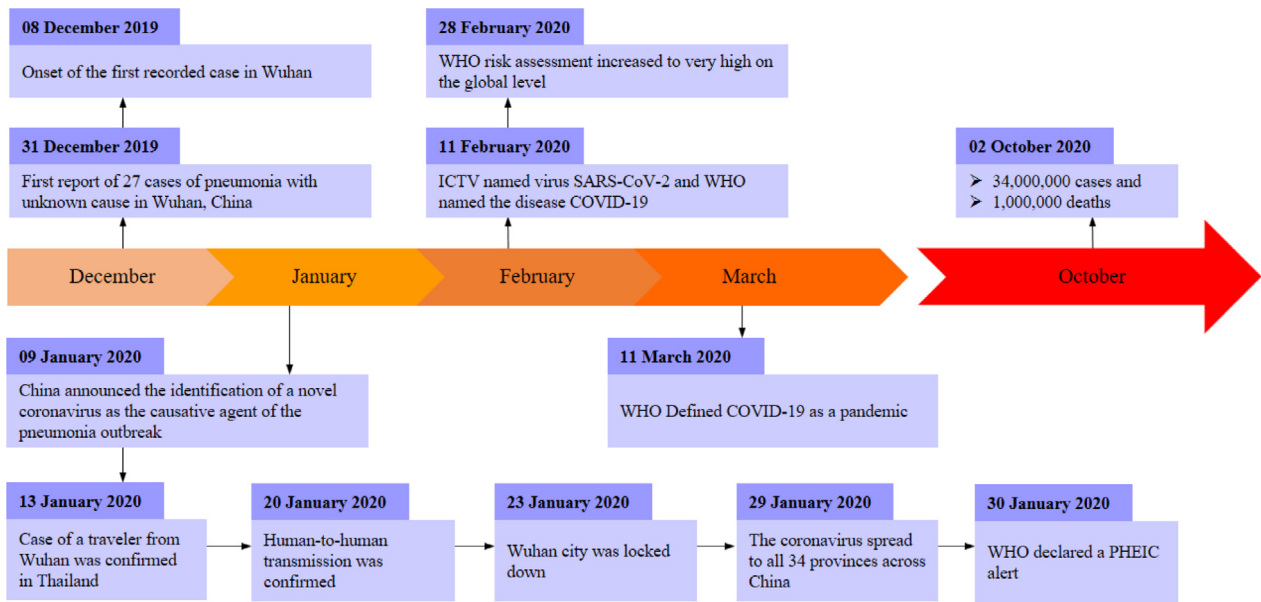


Fig. 1. Timeline of Covid-19 pandemic [1].

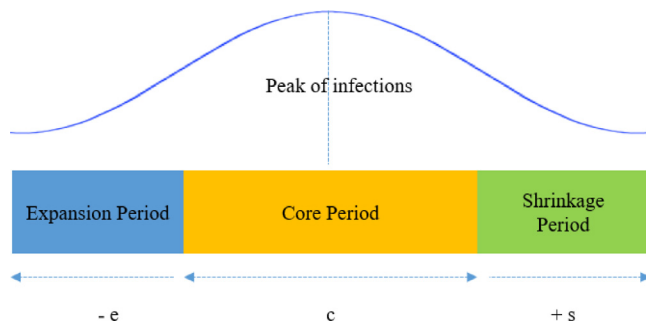


Fig. 2. The general structure of a wave.

can lead to discrepancies like underprepared infrastructure and lousy precautionary measures. Similarly, confusing a minor drop in counts with a downturn of the wave may lead to inconsistencies like a premature discharge of treatment and safeguards. Eventually, such inconsistencies result in a drastic loss of lives due to waves of new Covid-19 infections.

In this scenario, a well-defined demarcation of an upsurge or a downfall in a Covid-19 infection wave from temporary spikes or drops in the counts is critically essential. Hence, we propose an approach for detecting marker points among these spikes and drops. These markers enable us to forecast the behavior of an upcoming or ongoing wave of new infections with an observation window of minimum 7 days.

On a general note, the duration of a wave leads from an expansion period to a core and ends up with a shrinkage period (Fig. 2). The points where the expansion and shrinkage of wave initiates can be termed as up-trigger and down-trigger, respectively. Similarly, all points of rise in counts can be labeled as spikes, while the points of fall can be depicted as drops.

In this paper, we signify these triggers, spikes, and drops under a collective term called 'marker.' Detection of these markers will play a conclusive role in estimating the rise and fall of Covid waves in our proposed work. This estimation of each marker can be utilized for forecasting a specific behavior of Covid-19 waves (Table 1).

At the time of writing of this manuscript, the Omicron variant [5] of Covid-19 infection has surpassed all previous records

Table 1
Markers and their forecast interpretations.

Marker	Notation	Forecasted result
Up trigger	τ_{up}	Start of a new wave
Down trigger	τ_{down}	End of an ongoing wave
Spike	s	Rise in an existing wave
Drop	d	Fall of an existing wave

of infection cases triggering at least the third or fourth wave of infections in over 200 countries worldwide. Each wave of infections is composed of numerous temporary rises and falls in the infection counts. These rises and falls create a lack of transparency and generate severe confusion about the upcoming state of this pandemic. This confusion eventually worsens the situation and leads to the next wave of infections causing further damage. Thus, intensive research efforts are going on for cure [6,7], detection [8], and prevention [9] of Covid-19 disease. However, despite these efforts, any perceptible impact on this disease is unclear. This state of affairs has also motivated researchers to predict the upcoming state of Covid-19 in different regions of the world. Several works have been proposed on the forecast of infection counts [10] and duration of infection [11] within a brief span of time.

From simple iterations of confirmed cases [12] to dedicated computational models have been proposed for the projection and forecast of Covid-19 disease. The Susceptible–Infectious–Recovered–Dead (SIDR) model proposed by Fanelli et al. [13] employs a differential evolution algorithm for simulating the mean-field kinetics of the epidemic spread. Estimation of the basic reproduction number, case fatality, and case recovery ratios by Anastassopoulou et al. [14] is a further calibrated elaboration of such a model. Another instance of similar computational models is the SARI_qS_q model presented by Sarkar, Khajanchi & Nieto [15]. SARI_qS_q partitions the count of confirmed cases into susceptible (S), asymptomatic (A), recovered (R), infected (I), isolated infected (I_q), and quarantined susceptible (S_q) compartments to generate forecasts. A major section of the works on the Covid-19 forecast employs ARIMA modeling for [11,16] predicting upcoming counts in the future. Here, the researchers utilize the predictive performance of ARIMA models for projecting the specifics of Coronavirus infection in a region for a given span.

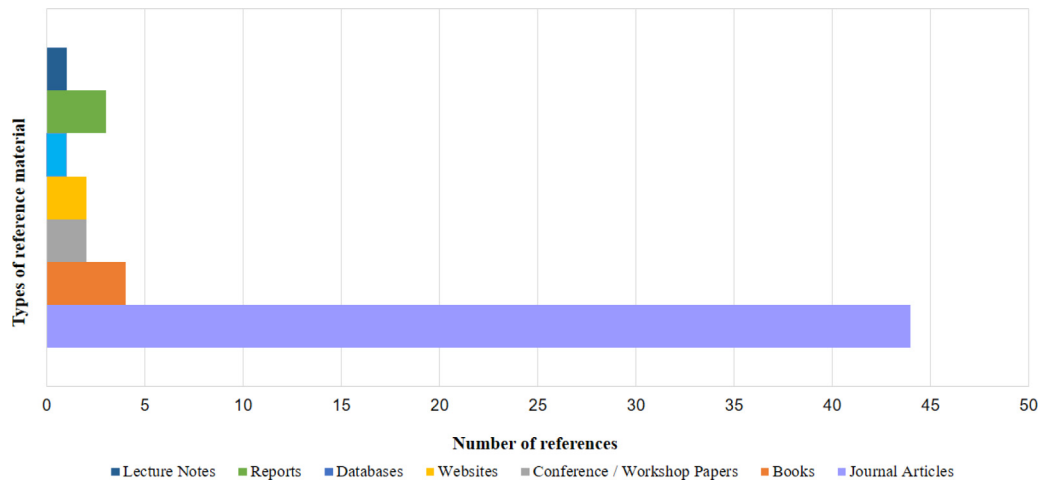


Fig. 3. Type and percentage of research literature referenced in this work.

However, as stated earlier, a wave of Covid-19 infections involves multiple sudden bursts of numbers. The inefficiency in handling these sudden data bursts is a significant limitation of ARIMA models [17]. ARIMA models generate linear patterns by corrective incremental adjustments over the autoregressive characteristics of the time series data. Such linear patterns generally fail to predict time series data that include multiple turning points [11]. Also, the dynamics of geography, climate, demography, and culture lay a serious impact on the behavior of a disease in a region. Likewise, the financial condition of the population, medical infrastructure, and especially the testing facilities play a decisive role in the epidemiological impression of the virus spread. Any mechanism that predicts on the basis of these fluctuating factors will be vulnerable to inconsistencies.

Furthermore, the proposed works stated in this section project the infection cases as a cumulative function of the factors discussed above. Only a few of them emphasize the temporal changes in the infection counts for an upcoming period. This fact also limits their efficiency in predicting the behavior of a wave of infection cases.

Therefore, we propose a framework of algorithms to forecast the behavior of a wave by detecting specific counts of new infections in a Covid-19 time series. We also propose to forecast the upcoming count of new Covid infections for the next day in a region.

1.1. Paper's contributions

The contributions of the proposed work can be summarized as follows:

Wave behavior forecast: We propose an algorithmic procedure to forecast the rise and fall of a potential wave of new infections by detecting the markers present in the timeline of Covid-19 infection cases in a provided region with an average forecast precision of 94.08%.

The procedure comprises a displaced double moving average (δDMA) technique and a decimal base shift function (β). The displaced double moving average (δDMA) generates the trend underlying a Covid-19 infection wave. By utilizing this trend, the decimal base shift (β) detects changes in infection counts that can be identified as potential markers of rise and fall in a wave of new infections. The determination of markers is guided by decision rules derived from the implementation of the rough set theory process on the Covid-19 time series data. These markers are later interpreted to forecast the upcoming behavior of a Covid-19 wave.

Infection count forecast: We further propose a novel algorithm for forecasting the upcoming counts of new infection cases in a time series data. The proposed algorithm is a variant of the single moving average method corrected by the addition of error gaps between the actual and projected values. Hence, we have named it as 'corrected single moving average (χSMA)' technique.

A framework of the algorithms proposed above has been implemented on time series data of new Covid-19 infections recorded in 12 different countries. We employ the walk-forward approach [18] for the execution of this framework on the time series data. This implies that the results of the proposed models get updated at every next input of new infection counts. The proposed work can be employed for the estimation of upcoming specifics of Covid-19 infections in a geographical region with an observation window period of 7 to 14 days.

1.2. Literature referenced

We have exhaustively referenced a sizable volume of literature from an extensive range of research works. Among these works, the ones based on the Covid-19 pandemic have been published from January 2020 to February 2022. The literature predominantly comprises reports, databases, lecture notes, websites, and books. But the chief constituent of this literature entails research articles from conferences and journals belonging to domains of computing, statistics, and medical expertise. The kinds and volume percentages of the different constituents of this literature have been summarized into a visualization presented in Fig. 3. The literature is entirely available in the public domain, and therefore no conflicts of interest have been discovered.

1.3. Paper's outline

The structure of the paper is as follows:

The literature background constituting the essential concepts and terminologies has been presented in Section 2.

Section 3 covers the problem statement, notations, data description, and formulated techniques under the proposed work.

Implementation of proposed techniques along with a case study of the first wave of Covid-19 pandemic in Australia is elaborated in Section 4.

Performance measures as well the analysis of results has been conferred over in Section 5.

Section 6 discusses various dimensions and assessments of the proposed approach.

The paper concludes with a summary of the proposed work and directions of possible future research.

2. Background

Before moving forward, we now discuss the prospective technical approaches that will serve as conceptual blocks for the design and development of the proposed forecast models. The architecture of these models is composed of moving average approach. A double moving average (DMA) variant of this approach combined with rough set-based decision rules is used for the detection of markers in a Covid wave. Likewise, a single moving average variant has been employed to forecast the infection counts for the next day. Thus, in this section, we discuss the specifics of rough sets and moving averages that comprise the architecture of the proposed forecast models.

2.1. Rough sets

Rough set theory can be viewed as a soft computing approach of uncertainty mathematics for mining structural patterns within incomplete, imprecise, and inexact information [19,20]. The concept of rough sets was introduced by Zdzislaw I. Pawlak in his landmark paper in the year 1982 [21]. A rough set is a generalization of classical set theory researched on the logical characteristics of information systems. They have been successfully applied in problem domains such as pattern mining, feature extraction, feature selection, and decision rule generation. Here we discuss a few definitions regarding the rough set theory relevant to our proposed approach.

Definition 1 (Information Systems). The rough set theory suggests the storage of input data in tabular designs called information systems. Each tuple of this information system represents a fact or an object which may be inconsistent with each other. Mathematically, any information system is expressed as a pair (U, C) where:

U (universe) = a non-empty finite set of all objects from the problem domain

C (attribute) = a non-empty finite set of conditional attributes such that $U \rightarrow V_c$ holds for every attribute $c \in C$. Here V_c should be considered the value set of attribute 'c'.

Definition 2 (Indiscernibility). Indiscernibility can be stated as the similarity of a set of attribute values for 2 or more given objects. As presented above, the information system table may consist of multiple objects (records) stored with similar feature values. Reducing the number of objects in this table can improve the efficiency of a proposed computational model. This reduction can be implemented by storing only the representative objects of every set with common features. Such representative objects are termed as indiscernible objects. Here, indiscernibility can be stated as an equivalence relation for the identification of these representative or identical objects.

Mathematically, for a set of attributes $P \subset Q$, an indiscernibility relation $IND(P)$ can be presented as:

$$IND(P) = \{(x, y) \in U^2 \mid \forall p \in P, p(x) = p(y)\}$$

This implies that the 2 objects x and y will be indiscernible by the set P of attributes in set Q , if $p(x) = p(y)$ for every attribute $p \in P$.

The sets of attributes that are indiscernible are also termed as elementary sets.

Definition 3 (Formal Approximations). We have discussed earlier that the rough set theory expands over the classical set theory. Therefore, the indiscernibility relation generates the following assumptions about an object 'x' in a set X belonging to the universe U (problem domain):

Assumption 1. Object x is in set X ;

Assumption 2. Object x is not in set X ;

Assumption 3. Object x is possibly in set X ;

These assumptions are defined on a crisp set (conventional set) by the following approximations:

Definition 3.1 (Lower Approximation (\underline{A})). A lower approximation can be specified as the set of domain objects that belong with certainty to the subset of interest. In simpler terms, it is the set of objects that positively belong to the target set. This implies that for a relation R , the lower approximation set (\underline{A}) of a given set X will be the set of all objects that can be linked to X with certainty regarding R given as:

$$\underline{A}X = \{X/[X]_A \mid A \subseteq X\}$$

Definition 3.2 (Upper Approximation (\bar{A})). The set of objects that possibly belong to the target set X can be considered as the upper approximation set. It is the set of objects that may belong to the subset of interest. For a relation R , the upper approximation set (\bar{A}) will be the set of objects which may be possibly linked to X given as:

$$\bar{A}X = \{X/[X]_A \mid X \cup X \neq \emptyset\}$$

Definition 3.3 (Boundary Region (A_b)). The boundary region (A_b) set describes the objects of a set X which can neither be classified under X nor as $\neg X$ with respect to a relation R . In other words, the boundary region covers the elements which may or may not belong to the target set X given as:

$$A_bX = \bar{A}X - \underline{A}X$$

In case the boundary region of set X is empty ($A_bX = \emptyset$), then the set will be considered as a classical or 'crisp' set with well-defined elements. This condition implies that all the objects are unquestionably covered under set X . Otherwise, with a non-empty boundary region ($A_bX \neq \emptyset$), the set X will be treated as a 'rough set'.

Definition 4 (Core & Reducts). Subsets of minimal attributes that can sufficiently characterize the complete knowledge of an information system are known as reducts. Attributes under reduct sets ($[A]_{Red}$) form equivalence class structures similar to those generated by the original set (X) of attributes. This condition is stated as:

$$[A]_{Red} = [A]_x$$

Similarly, the set of attributes common to all the reducts is termed as core ($[A]_{Cor}$). Mathematically, core attributes are given as:

$$[A]_{Cor} = \cap [A]_{Red}$$

The attributes present in the core set are central to all the reducts and cannot be removed from the information system without causing inconsistency in the structure of the equivalence class. The deduction of reduct and core sets provides a minimal subset consisting of attributes or features capable of providing information similar to that provided by the original dataset.

Definition 5 (Decision Rules). For a rough set, the minimal set of logical inferences or rules capable of characterizing the provided information system is termed as the set of decision rules. Under a given set of conditional features or independent variables $P = \{P_1,$

$P_2, P_3, \dots, P_n\}$ and a decision feature D , where $D \notin P$, the decision rules can be presented as:

$$R : (P_a = x_i) \wedge (P_b = x_j) \wedge \dots \wedge (P_c = \dots x_k) \rightarrow (D = x_m)$$

where $\{x_1, x_2, x_3, \dots, x_n\}$ are the feature values belonging to the domains of their respective features.

Such decision rules are expressed in the format of *IF cond[R] THEN dec[R]*. Here, the feature values compose the conditional part of the rule (*cond[R]*) presented on the left-hand side, while the decision part (*dec[R]*) forms the right-hand side of the rule. A decision matrix corresponding to each individual value (x) of the decision feature (D) is formed for the extraction of such rules. The decision matrix enlists all feature-value pairs that differ between objects included ($D = x$) and excluded ($D \neq x$) by the rule. The number of items present in the problem domain (U) that match the condition (*cond[R]*) is called the support for the rule. The rules meeting a threshold value of support are validated as final decision rules.

It should be noted that soft computing methods such as neural networks [22], fuzzy and rough sets [23] are generally used for decision-making preferences [24] in a data-intensive environment [25]. Here, the fuzzy sets and their generalizations [24,26] initiate processing by identifying a membership function a-priori and proceed to fit the data. However, the rough sets start fitting the data straightway into the preferences laid in the form of rules. Hence, we prefer rough sets better suited for this data-dependent scenario of the Covid-19 forecast, as any prior knowledge about the process is not required. The procedures of rough set theory that we have discussed above will be utilized for guiding the forecast generation process over the marker values present in the Covid-19 time series data. We will be employing moving average procedures for the detection of these markers and the patterns emerging from them. Thus, now we will elaborate on moving averages in the next section.

2.2. Moving average

A time series can be defined as an ordered set of quantitative observations of a phenomenon recorded at successive regular periods [27]. Such time-series data can be mined for useful patterns suitable for various applications. A forecast of upcoming values in a time series is an application of similar nature. Because of the wide utility of forecasts [28] in domains from stock markets [29] to electrical machines [30], several methods for the analysis of time series data have been proposed to date [31–34]. One such set of methods for forecasting future values in a time series is the moving average method [35,36]. Now we will discuss some variants of the moving average technique to be utilized in our proposed approach (Fig. 4.) for analysis of the time series data of new Covid infections in different regions of the world.

Definition 6 (Simple Moving Average). A Simple Moving Average (SMA) is the most commonly used variant of the moving average technique. It can be specified as the unweighted mean of previous k data points in a time series of n data entries. This implies that there are no weight factor values applied to any of the data points. In a series d_1, d_2, \dots, d_n of n data points, the mean of previous p points will be computed as SMA_p given in Eq. (1) as follows:

$$\begin{aligned} SMA_p &= \frac{1}{p} \sum_{i=n-p+1}^n d_i \\ &= \frac{1}{p} \left(\underbrace{d_{n-p+1} + d_{n-p+2} + \dots + d_n}_{\sum_{i=n-p+1}^n d_i} \right) \end{aligned} \tag{1}$$

In this equation, p denotes the count of data points or sub-group size [37] used in computation, while d_n represents the value of data point at period n . During each computation of values for succeeding data points, the new values will get added into the mean and the oldest ones will be dropped behind. This successive dropping and addition of values can be viewed as a moving transition of the SMA function through the time series (Fig. 4.). Hence, the technique is named as moving average. This successive computation of every next SMA for p points can be mathematically expressed in Eq. (2) as follows:

$$\begin{aligned} SMA_{p,next} &= \frac{1}{p} \sum_{i=n-p+2}^{n+1} d_i \\ &= \frac{1}{p} \left(\underbrace{d_{n-p+2} + d_{n-p+3} + \dots + d_n + d_{n+1}}_{\sum_{i=n-p+2}^{n+1} d_i} + \underbrace{d_{n-p+1} - d_{n-p+1}}_{=0} \right) \\ &= \frac{1}{p} \left(\underbrace{d_{n-p+1} + d_{n-p+2} + \dots + d_n}_{=SMA_{p,prev}} - \frac{d_{n-p+1}}{p} + \frac{d_{n+1}}{p} \right) \\ &= SMA_{p,prev} + \frac{1}{p} (d_{n+1} - d_{n-p+1}) \end{aligned} \tag{2}$$

In Eq. (2), we consider the sampling window of p points from $n-p+2$ to $n+1$ for calculating the next SMA of p points ($SMA_{p,next}$). In this manner, the oldest value of d_{n-p+1} is dropped and a new data point of value d_{n+1} is added to the sum with the previous SMA ($SMA_{p,prev}$).

Definition 7 (Double Moving Average). In addition to the definition specified above, SMA is also defined as the single moving average. This definition means that the averaging has been performed only once by the SMA function over a set of observed data points in a time series. But in the double moving average (DMA) technique, the moving average values are computed twice [37]. Here, the first average is computed on the original data points of the time series d_1, d_2, \dots, d_n of n data points. The next moving average is computed on the resultant values of single moving averages $sma_1, sma_2, \dots, sma_m$ of next m data points achieved in the previous step [38]. Hence, the double moving average, also known as dual moving average (DMA), can be considered as the moving average of SMA values. Computation of DMA from p number of precomputed SMA points has been presented in Eq. (3):

$$\begin{aligned} DMA_p &= \frac{1}{p} \sum_{i=m-p+1}^m sma_i \\ &= \frac{1}{p} \left(\underbrace{sma_{m-p+1} + sma_{m-p+2} + \dots + sma_m}_{\sum_{i=m-p+1}^m sma_i} \right) \end{aligned} \tag{3}$$

As this form of moving average is computed from a precomputed result in 2 stages, the noise and fluctuations of original data are also more flattened or smoothed in it compared to SMA. This smoothed data, free from noise and fluctuations, is generally useful for the projection of underlying trends in a time series.

Definition 8 (Displaced Moving Average). It is the periodically displaced variant of the traditional moving average in either a backward or forward direction in a time series chart. No additional computation is required for the displaced moving average beyond the calculation of its classical variants discussed above.

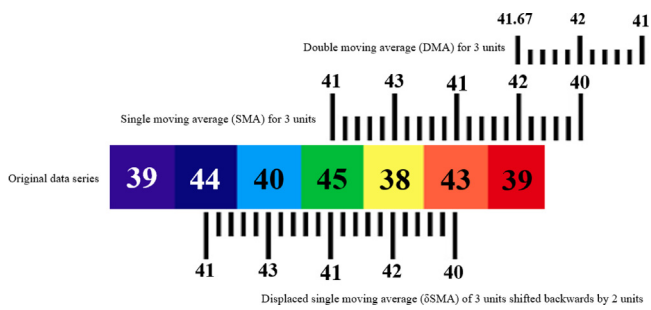


Fig. 4. Conceptual distinction of single (SMA), double (DMA) and displaced (δ MA) moving averages.

However, the average is simply shifted back or ahead of the data points by a specific window of periodic intervals.

A common usage of displaced moving averages is found in stock trading strategies [29] for better determination of market trends compared to usual moving averages [39]. The forward shift of moving average is termed as positive displacement and is presented by a rightwards movement of the values. Similarly, a negative displacement signifies a backward shift and is shown as a leftward transition of moving average values in the time series chart.

In the proposed work, we will be using a double moving average of 14 data points negatively displaced by an interval window of 14 units for projecting the current trend of the Covid-19 wave of new infections in a region.

3. Proposed work

In this section, we present our proposed approach with a detailed elaboration of components and process flow. We will first elaborate on the data utilized and later move towards the main work. But we initialize this section with the problem statement and the notations used.

3.1. Problem statement

Since its emergence, the count of new Covid infections has shown numerous spikes as well as drops in every region of the globe. These spikes and drops in the count have always created confusion about the future of this pandemic. This confusion has led to inconsistencies like underprepared infrastructure and lousy precautionary measures. Eventually, such inconsistencies have resulted into drastic waves of new Covid-19 infections. In this scenario, a well-defined demarcation of an uprise or downfall in a Covid-19 infection wave from temporary spikes or drops in the count is critically anticipated. Hence, we propose an approach for detecting marker points among these spikes and drops. These markers can enable us to forecast the behavior of an upcoming or ongoing wave of new infections with an observation window of minimum 7 days. Besides these markers, we also propose to project the upcoming count of new Covid infections for the next day with an average precision of more than 94% in a region.

3.2. Notations

As described earlier, our proposed model forecasts the rise and fall of a wave of Covid infections by detecting marker dates in the time series of infection counts. The model is composed of the following terms and notations:

C_i	Actual infection count on day i
$v[C_i]$	Range of new infection cases
n_t	Trend observation window (number of terms in one moving average for trend)
n_c	Count observation window (number of terms in one moving average for count)
w	Observation window (minimum number of days for which the count of new infections must increase)
δ	Displacement gap
M	Marker
τ_{up}	Up-trigger
τ_{down}	Down-trigger
s	Spike
d	Drop
β	Decimal base shift
χ_{SMA}	Corrected single moving average
δDMA	Displaced double moving average

3.3. Data description

The data utilized for the work proposed in this paper are obtained from the open-access resource of the 'Our World in Data' (OWID) repository [40]. OWID assembles and compiles the data from sources like the World Health Organization (WHO), Global Burden of Disease, World Bank, Johns Hopkins University, European Centre for Disease Prevention and Control (ECDC), and Blavatnik School of Government.

The data include and regularly update the date-wise confirmed counts of total infections, new infections, deaths, and vaccinations for 207 countries. To ensure geographic uniformity of data, our work employs the details of total and daily confirmed Covid-19 cases from 12 different countries, namely Argentina, Colombia, New Zealand, Australia, Cuba, Jamaica, Belgium, Croatia, Libya, Kenya, Iran and Myanmar. These details have been compiled into a time series database. The time series initiates from the date of a confirmed detection of the first case of Covid-19 infection in a region up to January 31, 2022. For example, the first confirmed case of Covid-19 infection in Argentina was detected on March 03, 2020, while the first infection in New Zealand was confirmed on February 28, and so forth. Hence, the respective time series of each country initializes on its own corresponding initializing date and extends to January 31, 2022.

Now, commencing with displaced DMA (δDMA), we discuss the components of our proposed forecast models.

3.4. Displaced DMA (δDMA)

For the time series data like a Covid wave, composed of several rises and falls in numbers, the determination of a trend can be challenging. To overcome this hardship, we employ displaced double moving average (δDMA), which forms the prime component of the proposed approach. We will be using it for tracking the trend of the Covid-19 infection wave by smoothing the time series data. δDMA is a combination of double moving average (DMA) and displaced moving average (δMA) techniques. We implement this displaced double moving average (δDMA) function by a procedure **ForecastTrend**.

3.4.1. Derivation of DMA

To achieve the target DMA values, the computation of single moving averages (SMA) is essential. So, we first compute the $SMA(14)$ of new infection counts throughout the time series for a trend observation window of 14 days as follows (Eq. (3)):

$$SMA_i(n_t) = \frac{1}{n_t} \sum_{i=j+1}^{j+n_t} C_i \quad (4)$$

where:

$SMA_i(n_t)$ = single moving average of next i th period

C_i = actual infection count on day i

n_t = trend observation window or the number of terms in one moving average for trend

Similar to $SMA(14)$, now we can derive the $DMA(14)$ of infection counts over the precomputed $SMA(14)$ values for the trend observation window of 14 periods given as:

$$DMA_k(n_t) = \frac{1}{n_t} \sum_{k=i+1}^{i+n_t} SMA_k \quad (5)$$

where:

$DMA_k(n_t)$ = double moving average of next k th period

SMA_k = single moving average value on day k

n_t = trend observation window or the number of terms in one moving average for trend

Here, we can note the different counter variables i , j , and k for SMA and DMA , respectively. These variables are included to ensure the distinct range of periods for single and double moving average values in every iteration.

3.4.2. Displacement of DMA

The $DMA(14)$ discussed above will generate a 'smoothed out' trend of new infection counts. However, these computed values of DMA will also appear 'forward shifted' in the time series chart by a gap equivalent to the subgroup size or observation window. This forward shift infers that each generated value of $DMA(14)$ will appear 14 periods ahead of the corresponding actual count in the time series chart. Thus, we need to drag the computed averages backward with the same duration (δ) of 14 periods to match the trend generated by $DMA(14)$ values with the current count of new infections in the region. Therefore, we implement backward displacement (δ) of DMA values by placing them δ number of points prior to their original positions given in Eq. (6) as follows:

$$\delta DMA_i(n_t) = DMA_k(n_t) \quad (6)$$

This procedure provides us an output trend vector ($T[D_i]$) comprising the difference of $\delta DMA(14)$ values computed over a trend observation window of (n_t) and displaced backward by a duration (δ) to match the current infection count (Eq. (6)).

$$T[D_i] = \delta DMA_i(n_{t+1}) - \delta DMA_i(n_t) \quad (7)$$

Throughout this section, we have denoted the number of terms or subgroup size [41] at each stage of the moving average as a trend observation window (n_t).

We have selected 14 days as the value of this window (n_t) for the DMA . Similarly, the displacement gap (δ) for a backward shift of the DMA values is also 14 days. The reason behind considering this duration for n_t and δ parameters is that the maximum proposed incubation period for Covid-19 infections is 14 days [42]. Because of this incubation period, the medically advised isolation or quarantine period for Covid-19 patients is also 14 days [43]. Within this range of time, any significant change in the state of the infected population will be visible. This change will be projected in the form of a peak, decline, or sustaining of numbers.

Hence, the procedure **ForecastTrend** generates the long-term trend ($T[D_i]$) of the infection counts by implementing the displaced double moving average (δDMA) for a trend observation window of 14 days. A positive increment in this trend will project a rise in the Covid-19 wave, while a decrement will depict a fall. Now we present the algorithm (Algorithm 1) for implementing the **ForecastTrend** procedure.

3.5. Decimal base shift

Detection of a marker date against a trend is our next target in the proposed approach. The marker must be robust enough to satisfy a conditional limit upon the count of newly infected population for a predefined timespan. Here, we will be utilizing the shift in decimal base (β) of infection counts as the proposed marker. By the term decimal base, we infer the number of digits present in a value. So, any difference or shift in the decimal base of new infection counts with a rising or dropping δDMA will be considered as a marker which includes up-trigger (τ_{up}), down-trigger (τ_{down}), spike (s), and drop (d). To compute this shift, we first need to retrieve the decimal base from the value of current infection count and then compute its difference from its predecessor value on the previous day. This section discusses the implementation of this shift (β) in the decimal base of infection counts as the **BaseShift** procedure.

3.5.1. Length of infection counts

As the infection counts are integer values represented in decimal form, so for retrieving their decimal base, we compute their logarithm in base 10. The value of an integer i composed of n digits lies between $10^{(n-1)}$ and 10^n . This implies that $\log_{10}(n)$ will fall between $(n-1)$ and n inclusive of both. Further, an addition of 1 to this value will provide the number (x_i) of digits as follows:

$$x_i = (\text{Log}_{10}(C_i) + 1)$$

The achieved value (x_i) will be in decimal format with a fractional component attached to its integer part. Therefore, we will now apply the floor function to cut down the fractional part, retrieving the actual length (n) as a result. Mathematically, this function is expressed as:

$$\text{Len}(x_i) = \lfloor x_i \rfloor$$

3.5.2. Shift in count length

After retrieving the length of the current infection count ($\text{Len}(x_i)$), we now need to detect any change in its decimal base from its previous values. Thus, this change or shift of base is computed as the difference of the current count length ($\text{Len}(x_i)$) and its adjacent predecessor ($\text{Len}(x_{i-1})$) given as:

$$\text{Base}(\beta_i) = \text{Len}(x_i) - \text{Len}(x_{i-1})$$

This approach has been presented in algorithmic format in Algorithm 2.

Now we elaborate our approach with an example. For the region of Australia, 75 new infections were witnessed on March 17, 2020. However, a count of 116 was observed on the next day, that is, on March 18, 2020. Now the logarithm of base 10 for 75 results into 1.87506. An addition of 1 to this number will provide 2.87506. In this number, the integer component is equivalent to the number of digits in 75, i.e., 2. However, the fractional component is no longer required and is hence truncated by the floor function. The final result will be 2.

Similarly, the value of logarithm of base 10 for 116 with an addition of 1 will be 3.06445, which, post truncation, will provide an integer value of 3. We will further compute the difference between the current and previous lengths to detect the change in count lengths. Here, a positive shift in base of 1 unit from 2 to 3 is visible between these 2 dates, which can possibly represent an up-trigger (τ_{up}) or a spike (s). Similarly, a negative shift can depict a down-trigger (τ_{down}) or a drop (d).

3.6. Corrected SMA (χSMA)

Forecasting the upcoming count of new infections in a region with high precision is a critical issue. This issue remains decisive


```

# Input: – Vector of new infection cases ( $v[C_j]$ ) of length  $max$ 
            – Value of trend observation window ( $n_t$ )
            – Value of displacement gap ( $\delta$ )

# Output: – Trend vector of computed  $\delta DMA$  values ( $T[D_j]$ )

ForecastTrend( $v[C_j]$ ,  $n_t$ ,  $\delta$ )
// Repeat procedure for a batch of next  $n_t$  infection counts up to length  $max$ 
for  $j = 0$  to  $max$ 

    // Compute single moving average ( $SMA_i$ ) for trend observation window  $n_t$  ( $n_t = 14$ )
    for  $i = j+1$  to  $j+n_t$ 
        
$$SMA_i(n_t) = \frac{1}{n_t} \sum_{i=j+1}^{j+n_t} C_i$$

        // Compute double moving average ( $DMA_k$ ) for trend observation window  $n_t$  ( $n_t = 14$  from  $SMA$ )

        for  $k = i+1$  to  $i+n_t$ 
            
$$DMA_k(n_t) = \frac{1}{n_t} \sum_{k=i+1}^{i+n_t} SMA_k$$

        end

        // Displace the computed double moving average ( $DMA_i$ ) upwards for day  $i$  by a shift gap of length  $\delta$  ( $\delta = n_t$ )
         $\delta DMA_i(n_t) = DMA_k(n_t)$ 

        // Trend generation from computed displaced double moving average ( $\delta DMA$ )
         $T[D_i] = \delta DMA_i(n_{t+1}) - \delta DMA_i(n_t)$ 

    end
end
return  $T[D_j]$ 

```

Algorithm 1: Implementation of the **ForecastTrend** procedure

```

# Input: – Vector of new infection cases ( $v[C_i]$ ) for  $i = 1$  to  $max$ 

# Output: – Value of decimal base change  $[-1, 0, 1]$ 

BaseShift ( $C_i$ )
// Compute value ( $x_i$ ) for count ( $C_i$ ) with logarithmic function of base 10 incremented by 1
 $x_i = (\log_{10}(C_i) + 1)$ 

// Compute length of count ( $C_i$ ) as the minimum integer value of value ( $x_i$ )
 $Len(x_i) = \lfloor x_i \rfloor$ 

// Detect the change in base ( $b$ ) or length of count ( $C$ ) between current ( $i$ ) and previous ( $i-1$ ) days
 $Base(\beta_i) = Len(x_i) - Len(x_{i-1})$ 

```

Algorithm 2: Implementation of the **BaseShift** procedure

in medical preparations and infrastructure buildup to combat the pandemic. To address this issue, the next goal of our proposed approach is to devise a novel variant of the moving average technique for generating the upcoming infection count for the next day with minimum error. We know that, generally, a gap always exists between the forecasted and actual values for every forecasting technique. This gap, termed as 'error,' forms the basis of various performance metrics for a forecast model like mean bias error (MBE), mean average error (MAE), mean square error (MSE), root mean square error (RMSE), and more.

We propose to utilize this gap to improve the efficiency of the moving average. Thus, we add the average of the errors attained at a stage of moving average to the value of the next stage. This addition can be considered as a form of 'correction' of moving average, hence named the 'corrected moving average (χMA)' method. This proposed correction aims to update the mean of a set of values with the average of the set of corresponding errors. Here, the average function evenly distributes any fluctuation in errors of the set, similar to as it does for the set of original values.

In this section, we will implement this approach on the single moving average (SMA) as the **ForecastCount** procedure (Algorithm 3), formulating the corrected single moving average (χSMA) for forecasting upcoming infection counts. The proposed approach accepts the vector of new infection counts ($v[C]$) and the value of count observation window (n_c) is set to 7 days for processing. Here, n_c denotes the number of values at a single stage of SMA similar to the trend observation window (n_t) of the δDMA model discussed in Section 3.4. However, the value of count observation window ($n_c = 7$) is accepted as half of the trend observation window ($n_t = 14$) to match the minimum incubation period for Covid-19 [42]. Here, n_c can be considered as the lower timeline limit of the incubation period to spot any changes in the state of the infected population. The proposed approach proceeds as follows:

3.6.1. SMA computation

In the first step of this method (Eq. (8)), we compute the SMA using the classical moving average technique by accepting

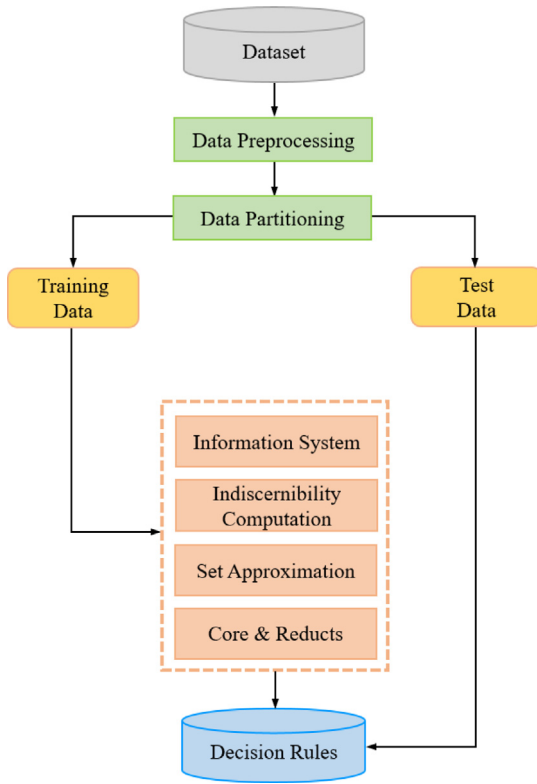


Fig. 5. Flowchart of decision rule generation process by use of rough sets.

7 values ($n_c = 7$) at every stage. This computation proceeds for the whole range or vector of new infection cases ($v[C_i]$). From this step, we will achieve the forecasted values of infections.

$$SMA_i(n_c) = \frac{1}{n_c} \sum_{i=j+1}^{j+n_c} C_i \quad (8)$$

3.6.2. Error determination

As discussed above, an error is expected to exist between the forecasted and actual values of infection counts. Thus, at this step, we compute the error (e_k) between count (C_k) and the single moving average value (SMA_k) for day k as:

$$e_k = C_k - SMA_k(n_c) \quad (9)$$

3.6.3. Average error

Now we compute the average of errors (E_i) retrieved for the n_c number of stages at stage i as:

$$E_i(n_c) = \frac{1}{n_c} \sum_{i=j+1}^{j+n_c} e_i \quad (10)$$

3.6.4. SMA correction

This step performs the main component of the proposed approach by adding up the error (E_k) attained at stage k to the moving average of stage $k+1$ (SMA_{k+1}) to generate a revised SMA ($Rev.SMA_{k+1}$) for the next day.

$$Rev.SMA_{k+1}(n_c) = SMA_{k+1}(n_c) + E_k \quad (11)$$

3.6.5. Absolute revised SMA

Finally, we compute the modulus of the revised moving average ($Rev.SMA_{k+1}$) to achieve the corrected single moving average (χSMA_{k+1}) as the forecasted number of cases.

$$\chi SMA_{k+1}(n_c) = |Rev.SMA_{k+1}(n_c)| \quad (12)$$

It should be noted that the addition of average error (E_k) to the next stage of SMA can also generate a negative value. However, the number of projected new infections cannot be negative in any case. Thus, this step is crucial for neutralizing any negative value of χSMA .

3.7. Decision rules generation

As discussed in Section 2.1 above, the detection of markers depicting any rise or fall in the trend of Covid-19 infections needs a guiding or filtering mechanism. This filter is provided by the decision rules generated from the provided Covid-19 database through the use of rough set theory. In this section, we will discuss the process of generation of these rules (Fig. 5). As discussed earlier, the rough set decision rules for any process are composed of conditional features $P = \{P_1, P_2, P_3, \dots, P_n\}$ and a decision feature D in the following format:

$$R : (P_a = x_i) \wedge (P_b = x_j) \wedge \dots \wedge (P_c = \dots x_k) \rightarrow (D = x_m)$$

Thus, the generation of decision rules is a process that requires the selection of appropriate variables from the information system. To set up the information system table from the provided Covid-19 database, we select the date and count of new infections (C_i) for every country under consideration.

1. Preprocessing

We now execute the **ForecastTrend** procedure to execute $\delta DMA(14)$ over the new infections (C_i) and generate the trend ($T[D_j]$). The trend will help in estimating the direction of the Covid-19 wave. Here, a positive value of $T[D]$ will project a rise in wave while the negative ones will present a fall. We also execute the **BaseShift** procedure to derive the decimal base shift (β) variable. Execution of these procedures can be considered under the preprocessing stage. This preprocessing sets the trend ($T[D]$) and base shift (β) as conditional features, while the marker (M) can be stated as the decision variable.

2. Data partitioning

We now partition our database into a 70:30 ratio of training and testing datasets for the 12 countries. As the count of infection dates differs for each country, the numbers of records in their training and testing datasets also differ.

3. Model generation

Now we compute the indiscernibility of attributes from the information system composed of the training dataset. We further calculate the set approximations to discard the conflicting records of the boundary region. The approximations lead us to discover the core and reduct attributes by estimating their dispensability. By utilizing the core and reduct attributes, we will mine the decision rules.

4. Validation

For a minimum observation window of 7 days, the decision rules are further validated against the records of the testing dataset with an accuracy of 96.4%. For trend value ($T[D]$), base shift (β), and observation window (w), the rules for marker (M) are as follows:

$$\text{if } ((b \geq 1) \ \&\& \ (T[D] \geq 0) \ \&\& \ (w \geq 7)) \rightarrow (M = \tau_{up}) \quad (13)$$

$$\text{if } ((M = \tau_{up}) \ \&\& \ (b \geq 1) \ \&\& \ (T[D] \geq 0)) \rightarrow (M = s) \quad (14)$$

$$\text{if } ((M = s) \ \&\& \ (b \geq 1) \ \&\& \ (T[D] \geq 0)) \rightarrow (M = s) \quad (15)$$

$$\text{if } ((b \leq -1) \ \&\& \ (T[D] \leq 0) \ \&\& \ (w \geq 7)) \rightarrow (M = \tau_{down}) \quad (16)$$

$$\text{if } ((M = \tau_{down}) \ \&\& \ (b \leq -1) \ \&\& \ (T[D] \leq 0)) \rightarrow (M = d) \quad (17)$$

$$\text{if } ((M = d) \ \&\& \ (b \leq -1) \ \&\& \ (T[D] \leq 0)) \rightarrow (M = d) \quad (18)$$

$$\text{if } ((b = 0) \ \&\& \ ((T[D_w] \geq 0) \ \text{OR} \ (T[D_w] \leq 0))) \rightarrow (M = \text{NULL}) \quad (19)$$

```

# Input: – Vector of new infection cases ( $v[C_i]$ ) of length max
– Value of count observation window ( $n_c$ )
# Output: – Corrected single moving average ( $\chi SMA$ ) as value of next infection case

ForecastCount( $v[C_i]$ ,  $n_c$ )
// Repeat procedure for a batch of next  $n_c$  infection counts up to length max
for  $j = 0$  to max

    // Compute single moving average ( $SMA_i$ ) for observation window of length ( $n_c = 7$ )
    for  $i = j+1$  to  $j+n_c$ 

        
$$SMA_i(n_c) = \frac{1}{n_c} \sum_{i=j+1}^{j+n_c} C_i$$


        // Compute the average error ( $E_k$ ) between count ( $C_k$ ) and single moving average ( $SMA_k$ ) for day  $k = j+n_c$ 
        
$$E_i(n_c) = \frac{1}{n_c} \sum_{i=j+1}^{j+n_c} e_i$$


        // Add the error ( $E_k$ ) to the  $SMA_{k+1}$  for generating revised  $SMA_{k+1}$  of next day
         $Rev.SMA_{k+1}(n_c) = SMA_{k+1}(n_c) + E_k$ 

        // Find the modulus of revised moving average ( $Rev.SMA_{k+1}$ ) to get corrected single moving average ( $\chi SMA_{k+1}$ ) as forecasted number of cases
         $\chi SMA_{k+1}(n_c) = |Rev.SMA_{k+1}(n_c)|$ 
    end
end
return ( $\chi SMA$ )

```

Algorithm 3: Implementation of the ForecastCount procedure

5. Decision filter

This rule base is implemented as a decision filter for the detection of markers by the **ForecastMarker** procedure. The rules can be summarized in the following manner. For the first positive base change (β) observed over a positive trend ($T[D]$) after an observation window of at least 7 days, an up-trigger (τ_{up}) will be marked. But all upcoming similar positive base changes observed after a τ_{up} will be recorded as spikes (s). Similarly, the negative base shifts (β) observed over negative trends ($T[D]$) after at least 7 days will be considered as down-trigger (τ_{down}) or drops (d). No marker will be considered if the decimal base does not change for a positive or negative trend. However, this condition does not imply the absence of a rising or deprecating infection wave.

4. Methodology

As discussed earlier, this approach is composed of moving average components and is directed by rules of rough set theory. So, in this section, we will discuss the methodology of implementing these components as an integrated assembly (Fig. 6.). This assembly is also presented in the algorithmic format in Algorithm 4. It receives the range of new infection cases ($v[C_i]$), count observation window (n_c), trend observation window (n_t), and displacement window (δ) as input.

4.1. System implementation

In the first step, the projected value of the new infection count for the upcoming day is forecasted by calling the **ForecastCount** procedure. This procedure executes χSMA function for a count observation window (n_c) of 7 days and generates an estimate of new infections for the next day. Further, a combination of δDMA and base shift is used for detecting spikes (s), drops (d), up-triggers (τ_{up}), and down-triggers (τ_{down}) by the procedure **ForecastWave**.

This procedure first determines a positive or negative trend of the Covid-19 infection wave by calling the **ForecastTrend** sub-procedure. Here, **ForecastTrend** returns a vector of $T[D]$ values as the trend for a provided range of infection counts. Further, the **BaseShift** sub-procedure detects changes in the decimal base

of the infection counts. After determining the trend and base shift, the **ForecastMarker** procedure executes the decision rules discovered by the rough set theory over the available Covid-19 database. For a provided observation window ($w = 7$), it classifies the -1 , 0 , and 1 values of **BaseShift** into markers as spikes (s), drops (d), up-triggers (τ_{up}), and down-triggers (τ_{down}).

Here, after passing the duration of the observation window of 7 days in a positive trend ($T[D]$) of infections, the very first point of any significant increase in count marked by the decimal base shift is termed as the first up-trigger (τ_{up}) depicted by an upward orange arrow (Fig. 7). The upcoming points of increase following τ_{up} can be regarded as spikes (s) shown by upward red arrows. Here, τ_{up} indicates the start of a Covid-19 wave while the spikes (s) forecast a further rise in an ongoing wave. In Fig. 7, the rise in wave forecasted by up-trigger and spike on February 29 and March 08, respectively attain the peak infection count of 497 cases on March 28. Similarly, with a negative $T[D]$, the first point of decrease in infections marked by a decimal shift is termed as a down-trigger (τ_{down}) displayed by a light green downward arrow. Also, further declines in counts are projected by drop (d) markers exhibited by downward dark green arrows. The fall of wave projected by the down trigger on April 07 leads to a further drop on April 22 to mere 07 cases. An up-trigger can be followed by multiple spikes displaying the increase in infection counts throughout the expansion period of an upward wave (Fig. 2). Similarly, several drops can follow a down-trigger representing the de-escalation of the wave. It must be noted that the direction of infection trend ($T[D]$) must favor the sign of **BaseShift** to be considered a marker. It implies that only a positive base shift observed after a positively increasing trend of minimum 7 days will be considered an up-trigger (τ_{up}) or a spike (s). A similar combination of a negative base with a negative trend will be stated as a down-trigger (τ_{down}) or a drop (d). However, a negative base shift parallel to a positive trend or vice-versa will not be considered the same as above.

4.2. Case study: First wave of Covid-19 infections in Australia

For further elaboration of our methodology, here we will discuss its implementation with the case study of the first Covid-19 wave in Australia [44].

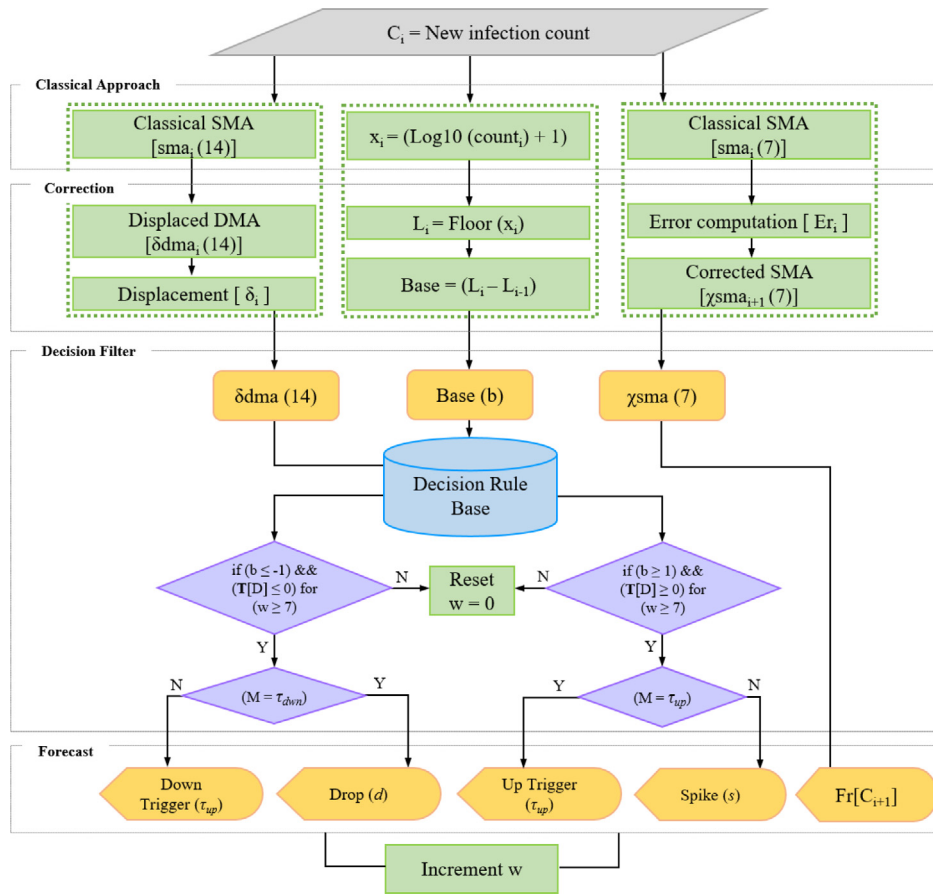


Fig. 6. Architecture of the proposed approach.

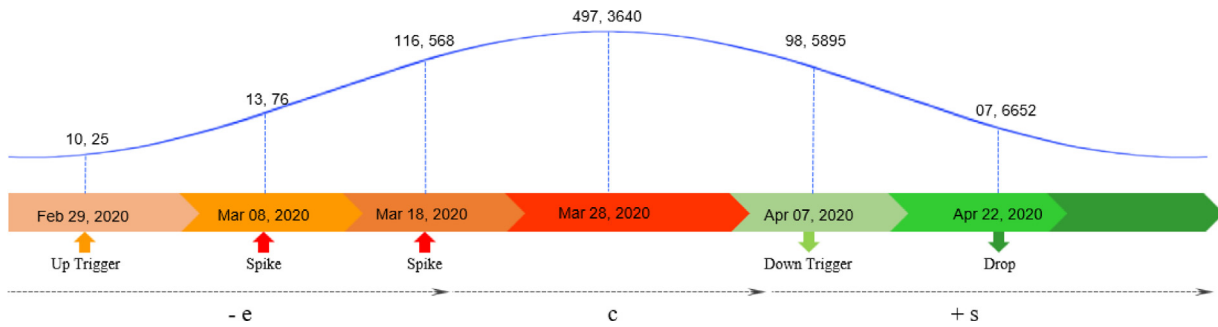


Fig. 7. Interpretation of the first Covid-19 wave in Australia.

In Fig. 7, we presented the details of various marker points consisting of up and down triggers, spikes, and drops in the first Covid-19 wave scenario in Australia. This scenario is further elaborated in the time series graph presented in Fig. 8. The graph depicts a series of different dates with changing new infection counts (C_i). Besides the new infection counts (C_i) presented by the blue line, 4 other lines are also present in the graph. These lines illustrate the trends computed from C_i through different moving average techniques. The orange and yellow lines present the trends of new infections retrieved by the $DMA(7)$ and $DMA(14)$ models. It must be noted that both of these lines are shifted ahead of C_i , which indicates the gaps between the real counts and the trends forecasted by these models. Similarly, the gray and violet lines running along with the infection count present the trends computed by $\delta DMA(7)$ and $\delta DMA(14)$ techniques. The trends are displaced backward by a displacement window of 7 and 14 days.

These displacements place the respective trends to match the actual counts, making them more relevant and valuable.

Now we elaborate the generation of markers against the trend of $\delta DMA(14)$ as presented in Fig. 9.

The first visible count of 04 infections was detected in Australia on January 26, 2020, with a decimal base range of 01. The $\delta DMA(14)$ function of our proposed approach retrieved the positive trend ($T[D]$) of value 0.0357 for the upcoming wave that started from February 17, 2020. Parallel to this positive trend, after crossing the count observation window of 7 days, the **BaseShift** procedure detected an up-trigger (τ_{up}) of 10 new infections on February 29 against a trend value of 0.5765. This up-trigger confirmed the start of the first Covid-19 wave in Australia. The next shift in decimal base with 13 new cases was spotted on March 08 as the forecast of the first spike of the upcoming wave. It was succeeded by another shift to the next decimal base range of 2 and recorded as another spike with an increase of

```

# Input: – Vector of new infection cases ( $v[C_i]$ ) for  $i = 1$  to max
            – Decision rule base ( $R_d$ )
            – Value of count observation window ( $n_c$ )
            – Value of trend observation window ( $n_t$ )
            – Value of displacement window ( $\delta$ )

# Output: – Trend vector of computed  $\delta DMA$  values ( $T[D_i]$ )
            – Corrected single moving average ( $\gamma SMA$ ) as value of next infection case

// Forecast new infection count  $Fr[C_{i+1}]$  for a batch of next  $n_c$  infections
Call ForecastCount( $v[C_i], n_c$ )
{
     $Fr[C_{i+1}] = \gamma SMA_{i+1}(7)$ 
}
end

// Execute following procedures for forecasting the behavior of a Covid-19 wave
ForecastWave( $C_i, n_c, n_t, \delta$ ) {

// Compute trend  $T[D_i]$  for a batch of next  $n_t$  infections
Call ForecastTrend( $v[C_i], n_t, \delta$ )
{
     $T[D_i] = \delta DMA_i(n_{t+1}) - \delta DMA_i(n_t)$ 
}

// Detect the change in base ( $b$ ) for current count  $C_i$ 
Call BaseShift( $C_i$ )
{
     $Base(b_i) = [-1, 0, 1]$ 
}

ForecastMarker( $T[D_i], C_i, b_i, w$ )
// Call decision rules from rule base and find for period of window ( $w$ ):

// if for a count decimal base if positive and trend is positive till  $n_c$  time window ( $w$ )
if ( $(b_i \geq 1) \ \&\& \ (T[D_{n_c}] \geq 0) \ \&\& \ (w \geq n_c)$ )
{
    // denote date as  $D_{up}$  and set marker as up trigger ( $\tau_{up}$ )
     $D = D_{up}$ 
     $Marker = \tau_{up}$ 
    Increment  $w$ 
}

// if for a count decimal base and trend are positive ahead of up-trigger
if ( $(Marker = \tau_{up}) \ \&\& \ (b_i \geq 1) \ \&\& \ (T[D_{n_c}] \geq 0)$ )
{
    // denote date as  $D_s$  and set marker as spike ( $s$ )
     $D = D_s$ 
     $Marker = s$ 
    Increment  $w$ 
}

// if for a count decimal base if negative and trend is negative till  $n_c$  time window ( $w$ )
if ( $(b_i \leq -1) \ \&\& \ (T[D_{n_c}] \leq 0) \ \&\& \ (w \geq n_c)$ )
{
    // denote date as  $D_{down}$  and set marker as up trigger ( $\tau_{down}$ )
     $D = D_{down}$ 
     $Marker = \tau_{down}$ 
    Increment  $w$ 
}

// if for a count decimal base and trend are negative ahead of down-trigger
if ( $(Marker = \tau_{down}) \ \&\& \ (b_i \leq -1) \ \&\& \ (T[D_{n_c}] \leq 0)$ )
{
    // denote date as  $D_d$  and set marker as drop ( $d$ )
     $D = D_d$ 
     $Marker = d$ 
    Increment  $w$ 
}

if ( $(b_i = 0) \ \&\& \ ((T[D_{n_c}] \geq 0) \ OR \ (T[D_{n_c}] \leq 0)) \ \&\& \ (w \geq n_c)$ )
{
    // denote date as  $D_{NULL}$  and set marker as neutral ( $NULL$ )
     $D = D_{NULL}$ 
     $Marker = NULL$ 
    Increment  $w$ 
}

// Reset the window ( $w$ ) for counting markers
else  $w = 0$ 
}
end

```

Algorithm 4: Implementation of the proposed system

counts from 75 to 116 on March 18, 2020. Similarly, the start of a negative trend in this Covid wave was depicted by the $\delta DMA(14)$ function on March 30 for 377 new cases with a reducing trend

($T[D]$) of -3.7092 . After passing the observation window of 7 days, the earliest negative shift from a decimal base of 3 to 2 was recorded as the first down-trigger (τ_{down}) on April 7 with 98

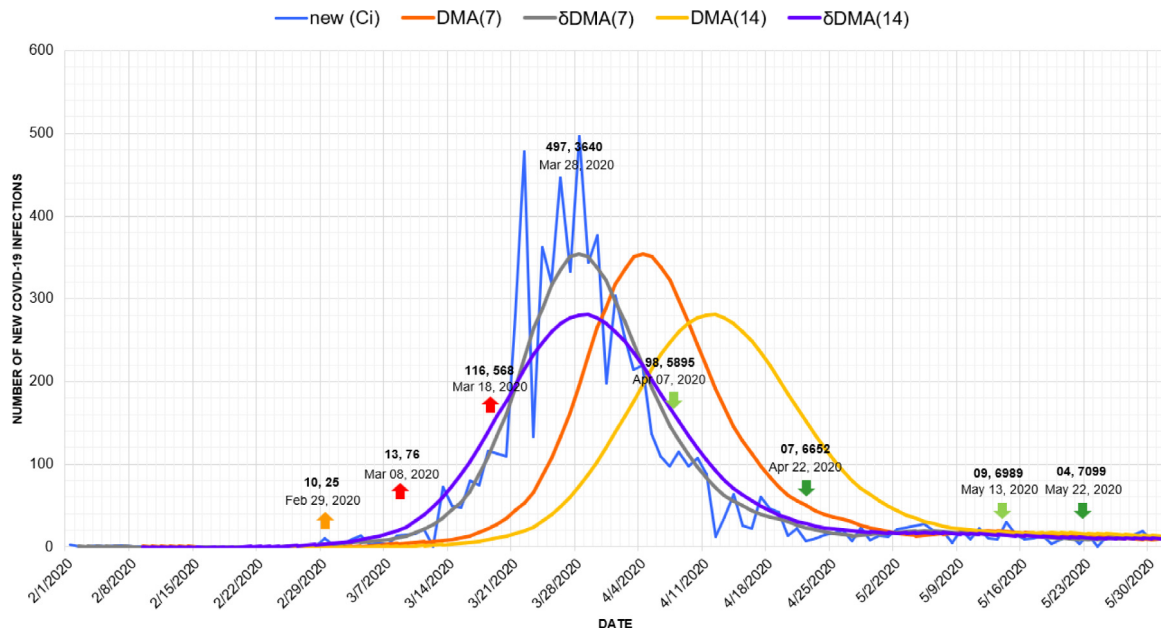


Fig. 8. Timeline graph of first wave of new Covid-19 infection cases in Australia.

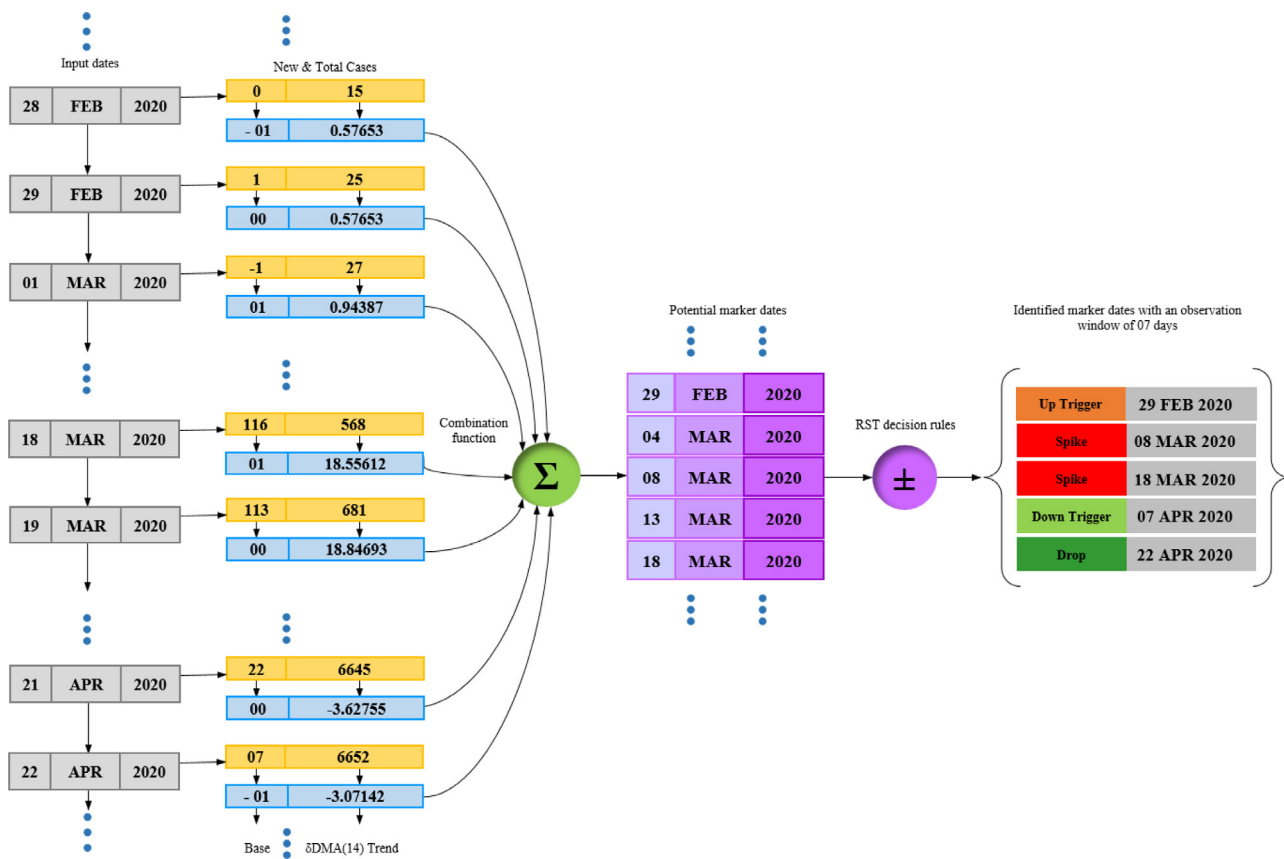


Fig. 9. Flowchart of marker detection from $\delta DMA(14)$ trend of a Covid-19 wave.

infections against a trend value of -16.4031 . This down-trigger was followed by a drop (d) of 7 more new infections on April 22, confirming the fall of the first Covid wave.

Regarding the forecast of the upcoming count of cases for the next day (Fig. 10), with respect to the actual 1701 witnessed on December 01, 2021, the $\chi SMA(7)$ function projected an approximate count of 1410 upcoming infections. Compared to the

results of the baseline techniques of $SMA(7)$ as 1362 with an error percentage of 19.926%, and $DMA(7)$ as 1364 with an error percentage of 19.85%, the $\chi SMA(7)$ forecasted with the lowest error of 17.139%. In terms of average mean bias error also, the $\chi SMA(7)$ performed the best with the lowest average error of 0.0389 compared to the average error of 7.785 of $SMA(7)$ and 16.147 of $DMA(7)$ baseline techniques.

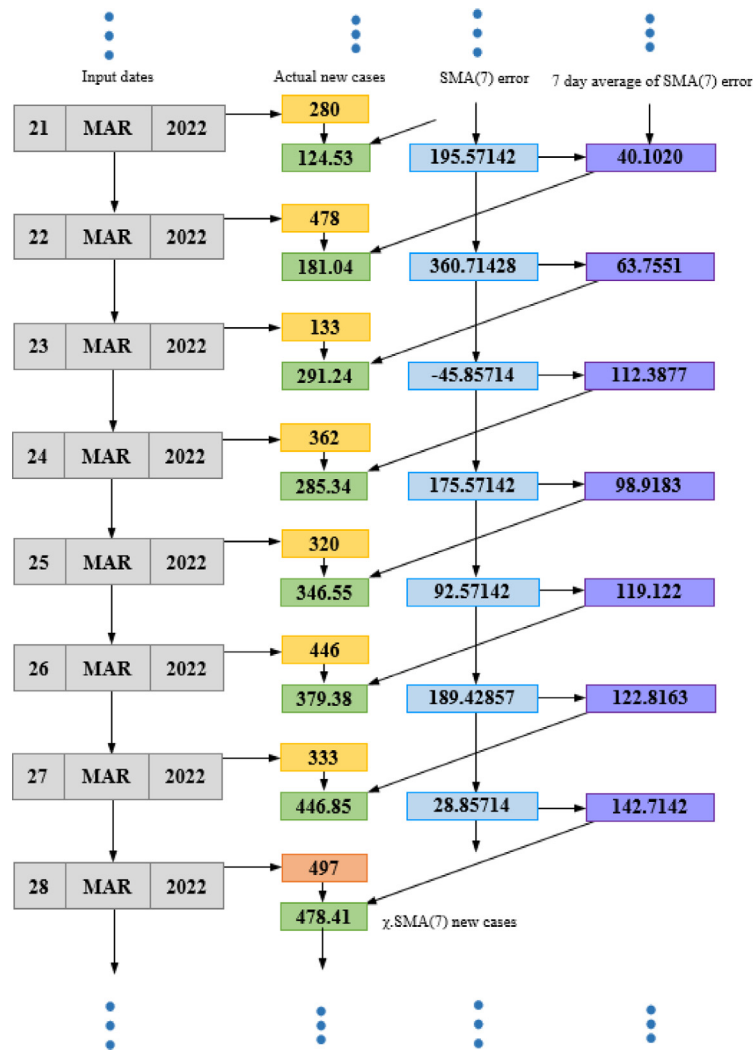


Fig. 10. Computation of upcoming infection count by χ SMA(7) function.

5. Experimental results

In this section, we will confer on the experimental details and results of the proposed approaches. But we will initiate this section with the performance measures that will be used to evaluate the efficiency of these approaches.

5.1. Performance measures

In our proposed work, the δ DMA(14)-base shift approach forecasts the behavior of the Covid-19 wave while the χ SMA(7) technique is focused on forecasting upcoming infection counts. Thus, we will be considering 2 distinct classes of performance indicators for evaluating the performances of the 2 proposed models. We commence this section with an elaboration of bias-based indicators.

Bias indicators: The mean bias error (MBE) and normalized mean bias error (NMBE) are the bias-based indicators to be used for the performance evaluation of the δ DMA(14)-base shift model. These indicators are based on the average error present in the values. This implies that strong chances persist of cancellation of positive and negative errors. This property of MBE is considered a major limitation that restricts its usage. However, we will be utilizing it here to measure the performance of the δ DMA models.

5.1.1. Mean bias error (MBE)

The difference between the actual (x_i) and the forecasted (y_i) value is termed as mean bias error (MBE). With n number of values or points, MBE can be mathematically stated as (Eq. (20)):

$$MBE = \frac{1}{n} \sum_{i=1}^n (x_i - y_i) \tag{20}$$

5.1.2. Normalized mean bias error (NMBE)

It is a normalization of the MBE indicator, which makes the results of MBE comparable by scaling them. NMBE computes the global difference between actual and projected values by quantifying the MBE through its division by the average of projected values (Eq. (21)).

$$NMBE = \frac{1}{n} \sum_{i=1}^n \left(\frac{x_i - y_i}{n} \right) \times 100 \tag{21}$$

Metrics like mean absolute error (MAE) and mean square error (MSE) defer the sign of errors to record the positive as well as negative errors also as positive quantities. This deferment of sign or direction, in turn, practically increases the final positive error manifolds and abandons the negative displacements altogether, losing the direction of the trend underlying the data.

Contrarily, MBE treats each error with its original positive or negative sign. Due to this property, strong chances of cancellation among positive and negative errors persist. This property of MBE is considered a major limitation that restricts its usage. However, in the case of the *DMA* models, our purpose is to project the trend visible in the time series data rather than forecasting the quantities with exactness. As MBE and NMBE are interrelated, we will be using both for the performance measurement of our *DMA* models.

We now proceed towards the description of precision-based performance indicators.

Precision indicators: Indicators based on precision specify the spread of the gap between the actual and forecasted values. But instead of positive or negative directions, these indicators measure only the magnitude of errors present in data. Here, the performance of the proposed *SMA* model will be evaluated by four different parameters [45], namely mean absolute error (MAE), mean square error (MSE), root mean square error (RMSE), and mean absolute percentage error (MAPE).

5.1.3. Mean absolute error (MAE)

The MAE measures the average magnitude of the errors in a set of forecasts without considering their positive or negative directions. This implies that the MAE is the average of the absolute values of the differences between forecast and the actual observation (Eq. (22)). The MAE can also be considered as a linear score which infers that all the distinct differences are equally weighted in the average.

$$MAE = \frac{1}{n} \sum_{i=1}^n |(x_i - y_i)| \quad (22)$$

5.1.4. Mean square error (MSE)

The average of squared differences between actual and forecasted values is computed by mean square error. In terms of regression, MSE states the proximity of a regression line to a set of error points. This proximity is calculated as the distances of error points relative to the regression line and squaring them removes any negative signs. Mathematically, MSE is stated as (Eq. (23)):

$$MSE = \frac{1}{n} \sum_{i=1}^n (x_i - y_i)^2 \quad (23)$$

5.1.5. Root mean squared error (RMSE)

RMSE can be considered as a quadratic score that measures the average magnitude of the error. Technically, it is defined as the square root of the squared difference among the forecasted (x_i) and observed (y_i) values of a quantity (Eq. (24)). Here, the squaring of errors before computation of their average allocates higher weights to large errors, thus projecting them distinctively. RMSE can be used in combination with MAE to detect the variations in errors among a set of forecasted values.

$$RMSE = \sqrt{\frac{\sum_{i=1}^n (x_i - y_i)^2}{n}} \quad (24)$$

5.1.6. Mean absolute percentage error (MAPE)

The mean absolute percentage error (MAPE) can be stated as the average of the absolute percentage errors of forecasts. Here, the percentage errors are totaled without considering their positive or negative signs.

$$MAPE = \frac{1}{n} \sum_{i=1}^n \left| \frac{x_i - y_i}{y_i} \right| \times 100 \quad (25)$$

In the next section, we will conduct an empirical analysis of the results of our proposed approaches over the Covid-19 time series database of 12 countries.

5.2. Empirical analysis

As discussed earlier, in this paper, we have analyzed the pandemic time series of 12 countries from their initial dates to January 31, 2022. Thus, in this section, we will inspect the results of the proposed work.

We constructed the χ *SMA*(7) model based on the single moving average (*SMA*) technique. The *SMA*(7) model forecasts the upcoming count of new Covid infections by computing the average of the infection counts for the previous 7 days. Its accuracy was improved by adding the average of residual errors derived as differences between actual and forecasted counts for an observation window of 7 days. This improvement fitted the χ *SMA*(7) model to the actual infection count with an average mean absolute deviation (MAD) of 787.61 compared to 859.66 for classical *SMA*(7) and 1081.369 as MAD for *SMA*(14). As the MAD of χ *SMA*(7) model is reduced significantly against the baseline models, consequently, the mean square error (MSE) and root mean square error (RMSE) are also reduced in a similar proportion. The minimum mean absolute percentage error (MAPE) of value 12.63 has been recorded for Iran by χ *SMA*(7) compared to 14.43 by *SMA*(7) and 19.33 for *SMA*(14) models, respectively. Likewise, the second minimum MAPE of value 16.10 was recorded by χ *SMA*(7) for Colombia against a MAPE of 17.48 by *SMA*(7) and 23.05 for *SMA*(14) models. In Table 2, we have compared the forecast errors as MAD, MSE, RMSE, and MAPE values generated by the 3 techniques over the time series data of new Covid-19 infections recorded in 12 countries.

We have further analyzed the count forecast performance of the proposed χ *SMA*(7) model against other baseline techniques. It should be noted that this projection can change with any upcoming count of new infections. Similar to the average forecast performance presented in Table 2, χ *SMA*(7) also outperforms its baseline counterparts in terms of daily count forecasts (Table 3). Here, χ *SMA*(7) resulted in a minimum average forecast error of 61% compared to 99.81% of *SMA*(7) and 137.49% of *SMA*(14). The best forecast of daily infection count (47.93) recorded for January 31, 2022, was projected by χ *SMA*(7) for Kenya with an error of only 4.21% against the actual count of 46 infections. In this case, χ *SMA*(7) presents significant improvements against errors of 243.47% by *SMA*(7) and 474.68% by *SMA*(14) models. In terms of a worst-case scenario of Croatia, the errors of 479.95% by *SMA*(7) and 484.68% by *SMA*(14) are still inferior to a lower error of 460.46% projected by χ *SMA*(7).

Now we evaluate the performance of the second proposed model of δ *DMA*(14) that projects the trend of Covid-19 infection waves. We will use mean bias error (MBE) to estimate the gap between the projected trend and the actual time series. Here, the trendline projected by the δ *DMA*(14) model fits nearest to the wave of infection counts (Table 4). This is depicted by the minimum MBE of 34.75 compared to MBE of 205.67 by *DMA*(7) and 439.68 by *DMA*(14) model. As a consequent indicator of MBE, the NMBE of δ *DMA*(14) also attains a minimum value of -3.356 against the 29.74 (*DMA*(7)) and 66.95 (*DMA*(14)) values. However, a negative NMBE represents that the trend of the proposed model is smaller than the original trend line.

It must be noted that the length of the displacement window among these models differs by a duration of 7 days. *DMA*(7) starts after 14 days, while δ *DMA*(7) initiates after 7 days of its parent *SMA* computation. This implies that δ *DMA*(7) has been shifted upward or backward in time series by a displacement of 7 units to match the wave of actual numbers. Similarly, *DMA*(14) starts without any backward displacement after 28 days. On starting with a displacement window of 14 units, this *DMA*(14) is portrayed as the δ *DMA*(14). The accuracy of this displacement is crucial to match the projections against the actual counts.

Table 2
Comparison of average forecast errors of χ SMA(7), SMA(7) and SMA(14).

COUNT	χ SMA(7)				SMA(7)				SMA(14)			
	MAD	MSE	RMSE	MAPE	MAD	MSE	RMSE	MAPE	MAD	MSE	RMSE	MAPE
Argentina	2630.207	36280918.6	6023.364	26.822	2923.695	51639878.73	7186.089	27.831	3542.809	90277202.18	9501.431	31.923
Colombia	1115.276	3535904.72	1880.4	16.101	1278.581	4750336.665	2179.526	17.481	1815.097	9327479.961	3054.092	23.059
New Zealand	7.763	242.763	15.580	52.886	8.016	256.757	16.023	47.894	9.863	371.085	19.263	54.054
Australia	1028.707	30953185.7	5563.558	38.786	1135.249	38333129.71	6191.375	42.693	1635.512	71543610.97	8458.345	55.774
Cuba	158.293	143672.781	379.041	29.089	195.420	189905.285	435.781	31.876	301.575	399625.924	632.159	40.823
Jamaica	57.252	13396.590	115.743	48.149	58.377	14744.85052	121.428	47.994	71.753	23214.111	152.361	54.938
Belgium	2455.838	54780112.8	7401.358	32.395	2489.568	53461698.4	7311.750	35.924	2734.681	57821300.81	7604.0318	44.334
Croatia	448.492	883089.751	939.728	71.769	473.069	888331.954	942.513	75.480	526.712	1032634.766	1016.186	85.496
Libya	229.245	208876.011	457.029	23.358	229.950	205674.495	453.513	21.547	248.930	237257.647	487.091	23.520
Kenya	149.255	71222.956	266.876	48.648	158.799	78814.079	280.738	51.013	190.701	120544.741	347.195	59.800
Iran	1055.076	4128910.12	2031.972	12.630	1230.285	5209738.468	2282.485	14.433	1702.150	8718068.397	2952.637	19.333
Myanmar	115.942	59437.671	243.798	39.250	135.022	84260.919	290.277	36.824	196.640	174582.349	417.830	45.320
	787.612	10921580.9	2109.871	36.657	859.669	12904730.86	2307.625	37.583	1081.369	19972991.08	2886.885	44.865

Table 3
Comparison of daily forecast errors of χ SMA(7), SMA(7) and SMA(14) recorded on January 31, 2022.

ERROR	COUNT on 31-01-2022	χ SMA(7)			SMA(7)			SMA(14)		
		For Count	For-Error	% For-Error	For Count	For-Error	% For-Error	For Count	For-Error	% For-Error
Argentina	43472	40202.979	3269.020	7.519	67521.142	24049.142	55.320	88594.214	45122.214	103.796
Colombia	15284	13115.142	2168.857	14.190	18828.285	3544.285	23.189	23441.5	8157.5	53.372
New Zealand	204	144.122	59.877	29.351	113	91	44.607	92.071	111.928	54.866
Australia	36719	51888.326	15169.326	41.311	54019.714	17300.714	47.116	58659.642	21940.643	59.752
Cuba	2119	2692	731.591	34.525	2937	915	43.180	3105.571	1038.928	49.029
Jamaica	410	437.326	27.326	6.665	648.142	238.142	58.083	848.857	438.857	107.038
Belgium	99314	52759.040	46554.959	46.876	51240.857	48073.142	48.405	46085.285	53228.714	53.596
Croatia	1445	8098.775	6653.775	460.468	8380.285	6935.286	479.950	8449.071	7004.071	484.710
Libya	4429	3819.346	609.653	13.765	2830.286	1598.715	36.096	1994.142	2434.857	54.975
Kenya	46	47.938	1.938	4.214	158	112	243.478	264.357	218.357	474.689
Iran	28995	19559.571	9435.428	32.541	13384.142	15610.857	53.839	8796.142	20198.857	69.663
Myanmar	278	197.755	80.244	40.577	169	109	64.497	150.714	127.285	84.454
				61.00074			99.813887			137.4955

Table 4
Comparison of trend projection performance by DMA(7), DMA(14) and δ DMA(14).

TREND	DMA (7)		DMA (14)		δ DMA(14)	
	MBE	NMBE	MBE	NMBE	MBE	NMBE
Argentina	772.1430356	19.54561898	1896.15562	33.58767343	139.3565127	-0.861120052
Colombia	229.2168405	15.30654897	527.1117111	26.60781529	51.56612062	-0.643813643
New Zealand	1.42425318	47.41597051	1.769185485	71.09265313	0.035457674	-7.441309463
Australia	590.8276047	31.89637674	1383.89143	113.5424323	225.6506074	-6.501396027
Cuba	34.05127664	20.29351115	67.87499615	36.76918559	4.690984086	-2.555473299
Jamaica	7.452019746	22.03676335	19.70685548	40.25481513	3.092397652	-2.574716535
Belgium	540.4560967	84.31176625	952.7358309	259.4170419	-6.12845481	-4.276487513
Croatia	90.8856495	36.17748388	175.7354829	70.3852792	1.903376815	-4.753484139
Libya	34.3157281	28.42878751	47.0839368	52.09404609	-1.42451174	-3.288684683
Kenya	1.851074749	17.10181175	7.27152568	37.23975243	2.179380665	-2.403374823
Iran	163.2725468	10.07760268	193.2607404	13.71961639	-4.03123045	-0.838485678
Myanmar	2.151119058	24.39752169	3.576310154	48.72693533	0.226001512	-4.1398242
	205.6706038	29.74914696	439.6811354	66.95310385	34.75972018	-3.356514171

6. Discussions

This section will discuss various aspects and challenges met in this manuscript and their plausible answers in terms of component techniques, functional specifics, and results.

6.1. Comparative analysis

Continuing from the results of the previous section, here we present a comparison of the various approaches on Covid-19 forecast (Table 5). We also compare our proposed approach against these approaches. We can broadly categorize the works discussed in this manuscript into ARIMA-based and Compartment-based

approaches. As the name suggests, the ARIMA technique comprises the major algorithmic component of the ARIMA-based approaches [10,11]. On the other hand, every compartment-based approach partitions the population of the region under consideration into compartments like susceptible (S), infected (I), recovered (R), and dead (D) populations for the generation of models [13–15], hence the name.

Another category under which Covid-19 forecast applications can be placed, is the category of model-based approaches. These approaches comprise logical or mathematical models for structuring the forecast on the basis of population counts [12]. We place our proposed approach under this category. The forecasts on the rise and fall of the waves of infection counts form the primary

Table 5
Comparative summary of selective works on Covid-19 forecast.

Reference	Year	Data	Constituent technique	Proposed work	Advantages	Limitations
ARIMA-based approaches						
[10]	2020	Italy, Spain, Turkey	Auto Regressive Integrated Moving Average (ARIMA), autocorrelation function (ACF), partial autocorrelation (PACF)	Predicting the number of cases and deaths from time series data.	Month-wise forecast of infection and death counts.	1. Complex selection of p, q, r parameter values for appropriate ARIMA model. 2. Counts saturate after a threshold time.
[11]	2020	India, Brazil, Spain, Russia, United States	Auto Regressive Integrated Moving Average (ARIMA), Hannan and Rissanen algorithms.	Predicting the number of cases and deaths from time series data.	Count-wise and month-wise forecast of infection cases.	1. Complex selection of p, q, r parameter values for appropriate ARIMA model. 2. Counts saturate after a threshold time.
Model-based approaches						
[12]	2020	United States, Slovenia, Iran, Germany	Simple iteration of infection counts for a specified number of days	Determination of the average growth rate of infection from daily values of confirmed cases.	Simple implementation	1. Based on infection growth rate. 2. Provision for only first insights of the pandemic 3. Accuracy is not assured
Compartment-based approaches						
[13]	2020	China, Italy, France	Differential evolution algorithm implemented on mean-field kinetics of the epidemic spread.	Modeling of susceptible (S), infected (I), recovered (R), dead (D) population counts.	1. Model captures gross features of the outbreak. 2. Simple implementation	1. Assumes that counter measures must cause a quick and effective reduction in infection rate. 2. Counts saturate after a threshold time.
[14]	2020	China	Linear regression modeling	Estimations of the basic reproduction number (R_0) and the per day infection mortality and recovery rates on the basis of SIDR model.	Flexible and elaborate implementation	Assumption of the count of infected and recovered populations to be 20 and 40 times respectively, relative to the actual counts, leading to possible gaps in results.
[15]	2020	India	Nonlinear differential equation modeling	Modeling of susceptible (S), asymptomatic (A), recovered (R), infected (I), isolated infected (I_q), and quarantined susceptible (S_q) population counts.	1. Model captures multiple features of the outbreak. 2. Simple implementation	1. Dependent on a predefined set of parameters. 2. Lacks sensitivity to change in infection counts.

component of our approach, which is not addressed by any other work. These forecasts on the behavior of infection waves form the major distinction of our proposed work from the approaches discussed here. Apart from simple implementation, the execution of our approach is also independent of any dynamic parameter, such as infection or recovery rates. Hence, in broad terms, it can be employed for modeling any epidemic over any specified geographic profile and population. Further, we have implemented our approach on an extensive range of population counts from 12 different countries. Also, the discussed approaches forecast on the upcoming waves up to the accuracy of months for a provided region. Contrarily, our proposed model is capable of forecasting the behavior of an infection wave with a sensitivity of 7 days. Similarly, it also forecasts the upcoming counts of new infections under a minimum observation window of 7 days with high accuracy.

6.2. Results per country

As described earlier, including the case study of the first Covid-19 wave in Australia, we have analyzed the Covid-19 infection data of 12 countries. Hence, here we will confer upon the results achieved by implementing the proposed approach over the data of these countries.

The prime observation of these countries is that the infection counts due to the Omicron variant of Coronavirus have surpassed all the previous numbers. The wave caused by Omicron variant has led to the suppression of preceding waves in the time series

graphs of these countries. Now we will elaborate on the individual observations for each country along with their time series graphs in this section.

In South America, Argentina depicts a perceptible rise and fall of 3 waves (Fig. 11). However, due to the local spikes and drops, the fall of the first wave was not marked evidently, and the second wave initiated from it on March 26, 2021, with 12,936 new infections. Here, considering that the major number of infection cases was imported, decisions like closing borders, establishing quarantine, and canceling flights helped Argentina to sustain better during the first wave [46].

On the other hand, Colombia is among the worst-hit South American nations by Coronavirus. Here, the markers of our proposed approach have detected the explicit behavior of each wave. Surprisingly, the third wave, marked from April to September 2021, was undeniably as devastating as the fourth wave (Fig. 12.). Improper timing of pandemic responses like vaccination and instituting unpredictably long lockdowns have been plausible reasons for the distressing state of the pandemic in Colombia [47]. Nevertheless, similar to Argentina, the second wave initiated from the minor drop of the first wave on October 29, 2020, with 11,187 new infections.

In the region of Oceania, New Zealand managed to control the pandemic successfully after the first wave marked from March to May 2020. In addition to measures like adequate testing, timely procurement of medical supplies, closure of schools, sealing of borders, and social distancing made a positive impact. Here, a 4-level risk assessment system helped the New Zealand administration significantly to respond to the pandemic in a

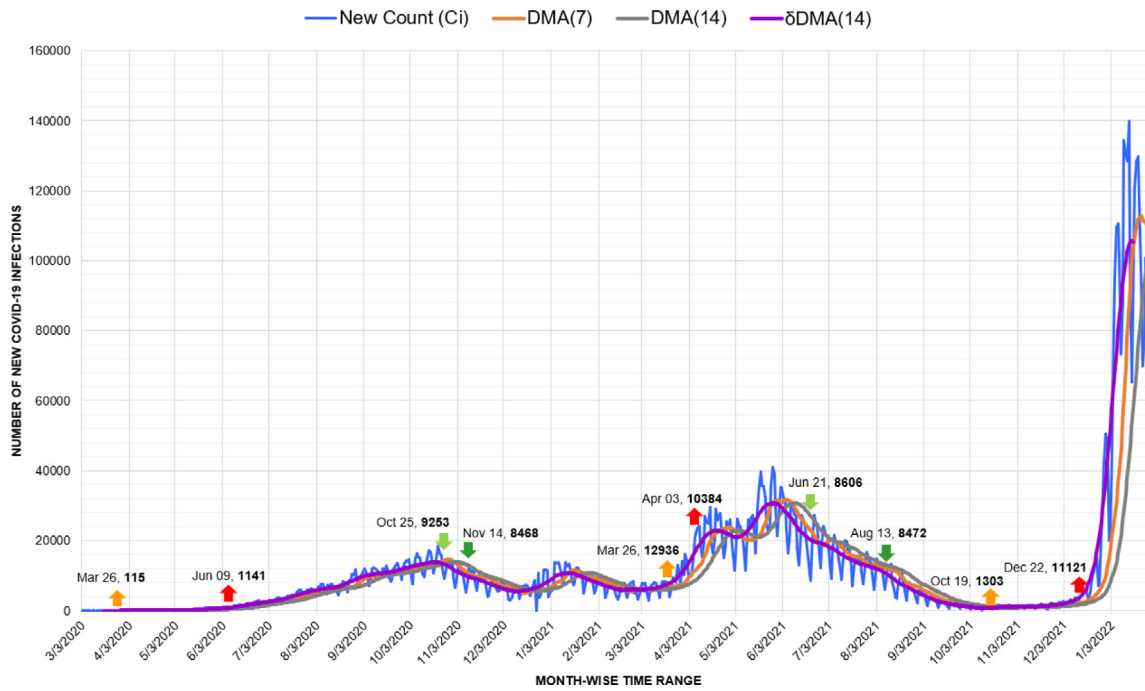


Fig. 11. Timeline graph of new Covid-19 infection cases in Argentina.

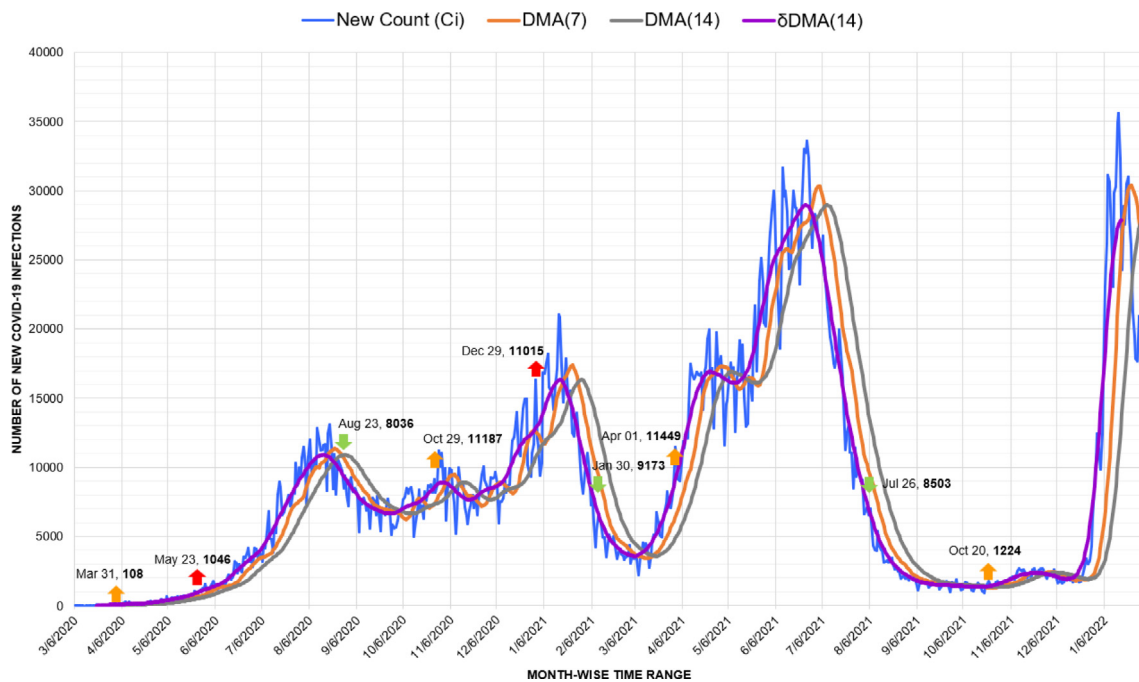


Fig. 12. Timeline graph of new Covid-19 infection cases in Colombia.

strong and efficient manner [48]. The system facilitated suitable categorization of the risk due to the pandemic and aided the implementation of clear and well-specified public health measures at each level. Therefore, the peaks witnessed in January 2021 after the first wave were still much lower than the first wave. Though, the wave caused by the Omicron variant with a spike on October 28, 2021, due to 129 cases, surpassed previous efforts (Fig. 13).

Australia exemplifies one of the stark instances of the suppression of previous waves due to the rise in counts caused by the Omicron variant. As visible in Fig. 14, the peaks of the first and second waves observed in March and June of 2020 had merely 18 and 27 new counts, respectively. Similarly, the peak in March

2021 witnessed the highest count of 12 cases. Synonymous with New Zealand, in Australia also, geographic isolation, relatively higher testing rates, and early implementation of social distancing measures were among the potential factors of successful response [49]. Yet, later these figures transmuted to a flat line against the trigger of 11,797 infections recorded for the fourth wave in December 2021.

In Cuba, Covid-19 infection arrived with 3 Italian tourists in March 2020. With prompt sealing of borders, mandating face masks, and isolation of the infected population, Cuba responded to the pandemic successfully till November [50]. But, later, a nominal up-trigger of 104 cases observed on December 05, 2020,

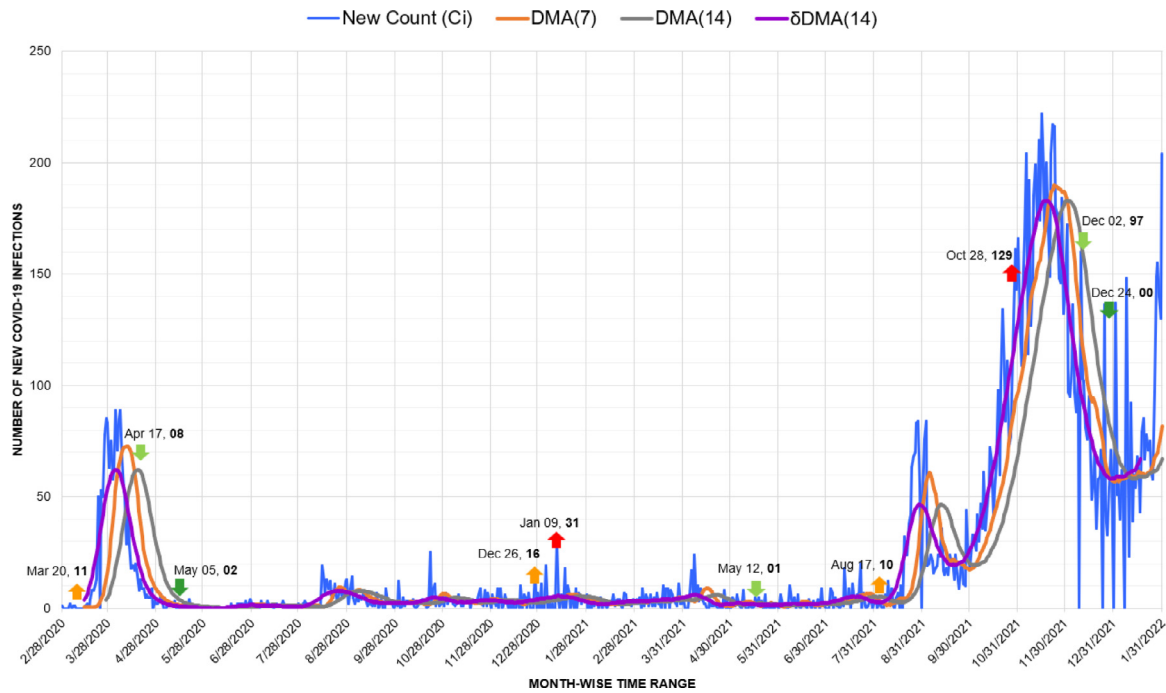


Fig. 13. Timeline graph of new Covid-19 infection cases in New Zealand.

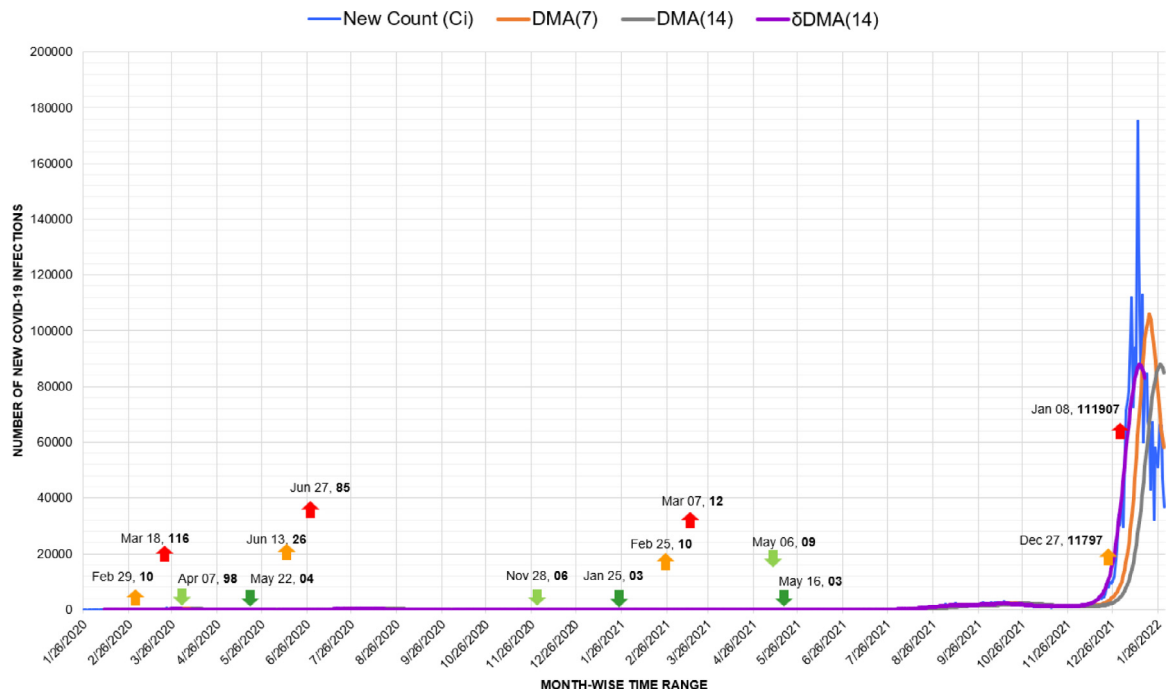


Fig. 14. Timeline graph of new Covid-19 infection cases in Australia.

erupted into a devastating wave from June to December 2021 (Fig. 15). Here, the shift of decimal base was recorded as an up-trigger of 1008 cases on March 30 and a spike of 1047 cases on April 09, 2021.

Before the first minor spike of 10 cases on 22 April, Jamaican authorities advised wearing masks only for persons over 65 years and individuals with symptoms or respiratory vulnerabilities [51]. Due to such misjudged policies, similar to Colombia, Jamaica also

observed clear phases of Covid-19 waves, with each wave surpassing the records of the previous ones. The markers of our approach effectively depicted the triggers, spikes, and drops of each wave. Here also, the Omicron variant caused an unprecedented spike of 1128 infections in January 2022 (Fig. 16).

In Belgium, after responding successfully to the first peak, the start of educational year in academic institutions and the return of summer tourists from across the borders initiated the peak of October 2020 [52]. However, alike Australia, Belgium presents another case of suppressed previous waves by the latest wave in

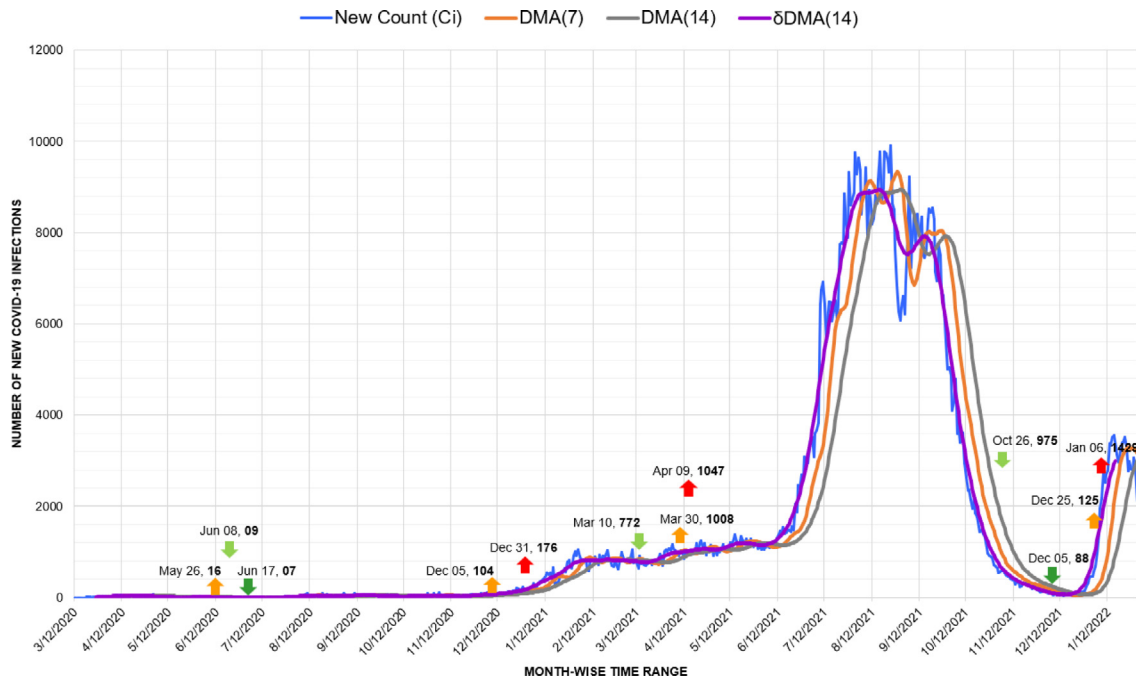


Fig. 15. Timeline graph of new Covid-19 infection cases in Cuba.

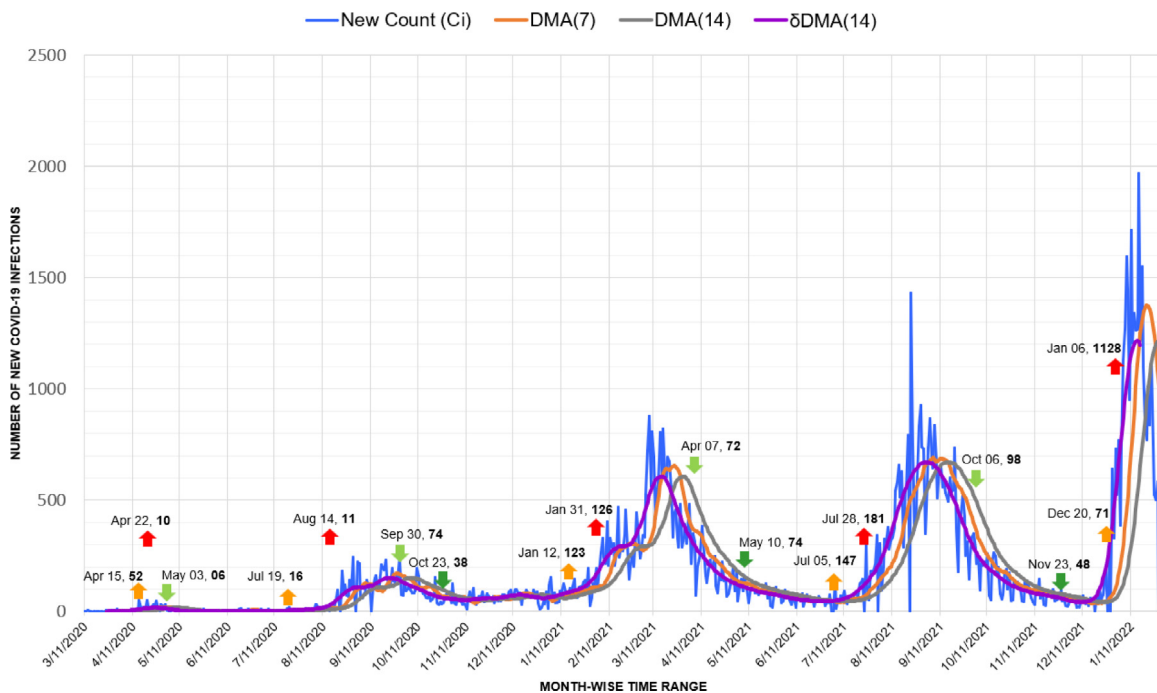


Fig. 16. Timeline graph of new Covid-19 infection cases in Jamaica.

January 2021 (Fig. 17). Against a trivial spike of 1298 infections in March 2020, the trigger of 27,941 cases recorded in January 2021 resulted in an unprecedented Covid infection wave.

One of the most evident utilization of the trend generated by the $\delta DMA(14)$ model can be seen in the time-series graph of Croatia. Similar to New Zealand, the Croatian administration also employed a crisis management system for assessment and decision-making during the pandemic [53]. Here, extreme fluctuations are visible throughout each Covid-19 wave. These fluctuations indicate the rise of counts on one day and a sudden drastic

drop within the next few days (Fig. 18.). The trends generated from these fluctuations have been analyzed appropriately by the $\delta DMA(14)$ model. The last and the highest wave in Croatia was recorded with an up-trigger of 4139 cases on December 28, 2021.

Due to increased transmission vulnerability, political instability, and an inferior infrastructure for food and medical facilities, Libya has been placed among high-risk zones of the Covid pandemic [54]. Consequently, a significant observation in Libya was multiple drops to zero infection cases in many waves. A plausible

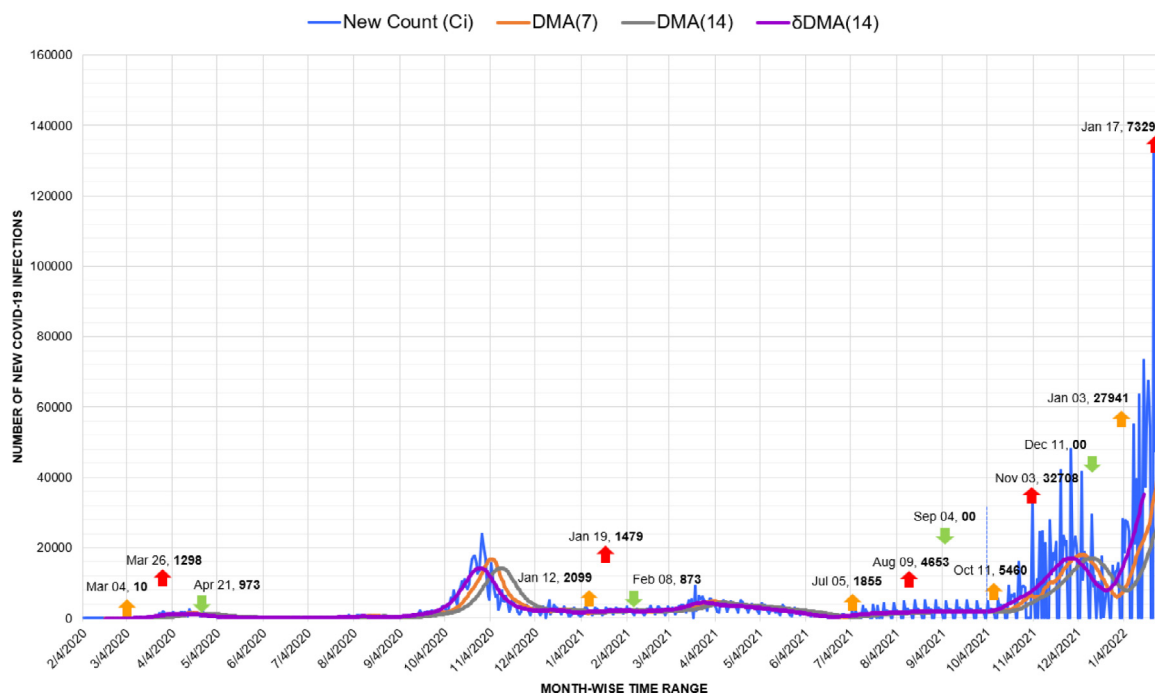


Fig. 17. Timeline graph of new Covid-19 infection cases in Belgium.

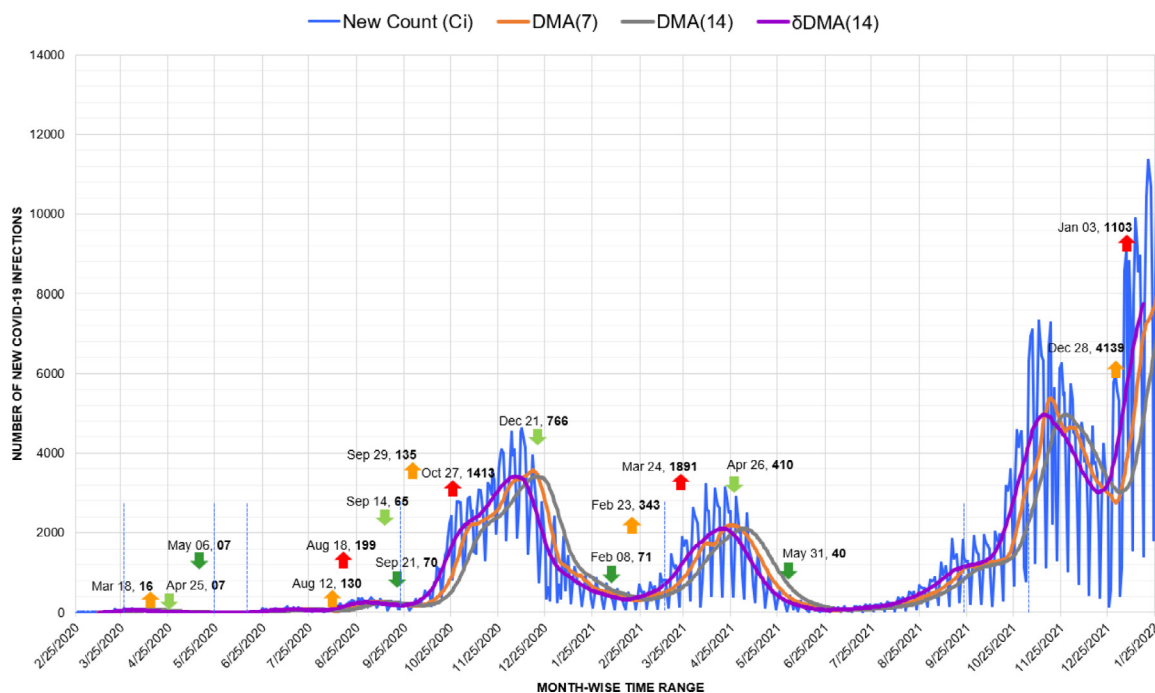


Fig. 18. Timeline graph of new Covid-19 infection cases in Croatia.

reason for this absence of numbers may be the lack of information or the deficiency of medical testing facilities in the region. However, our $\delta DMA(14)$ model could still map a well-matched trend against these fluctuating counts. Until the writing of this manuscript, the latest and highest wave of infections was in its initial rising phase in Libya (Fig. 19).

Kenya can be viewed as a case with the most evidently visible Covid-19 infection waves. Similar to Jamaica, every wave in Kenya shows a clear rise and fall of counts to visible limits in time series.

Each wave has been marked with triggers, spikes, and drops by our approach (Fig. 20). Here, the third and fourth waves recorded a similar extent of damage, while the fourth wave depicted the highest count of 741 new infections on January 09, 2022. However, in addition to the nationwide educational media campaigns for promoting the usage of masks and handwashing, the Kenyan government also provided financial support to the local informal business sector for establishing sanitization mechanisms and handwashing stations through recycled and raw materials [55].

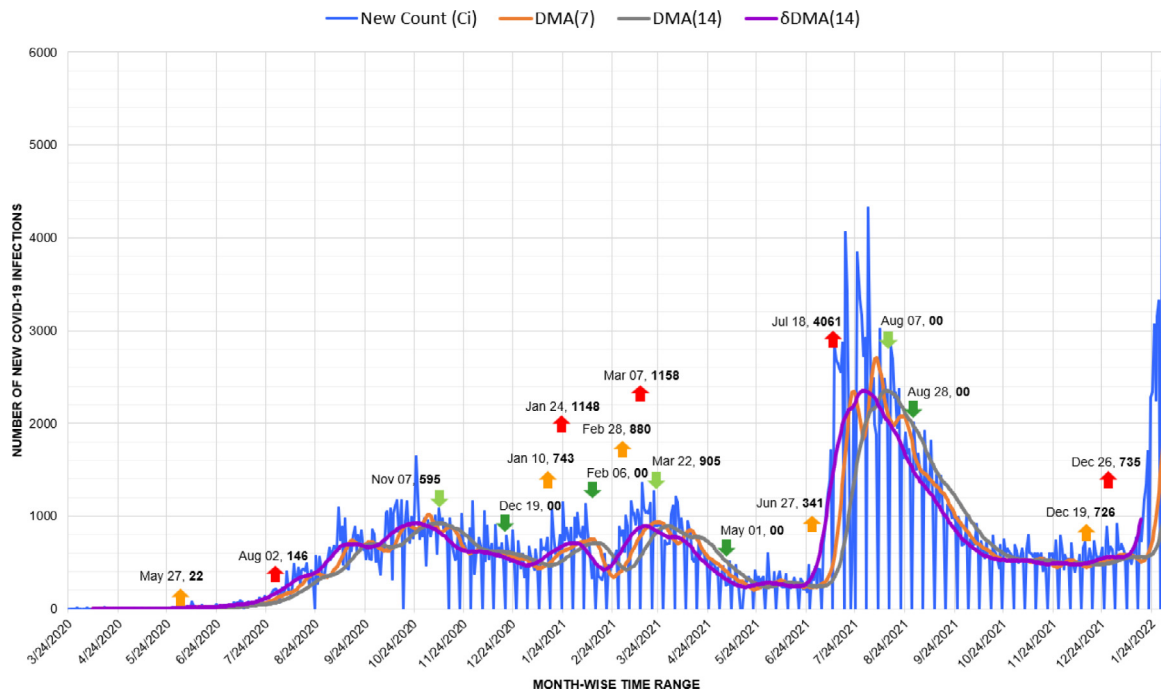


Fig. 19. Timeline graph of new Covid-19 infection cases in Libya.

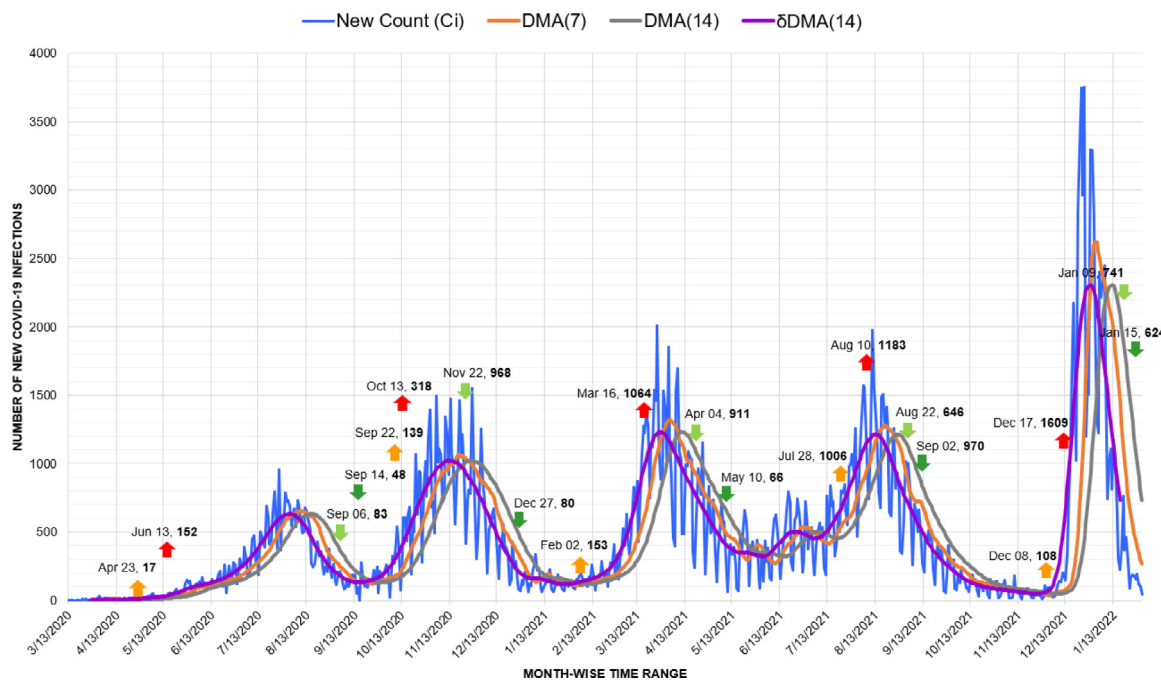


Fig. 20. Timeline graph of new Covid-19 infection cases in Kenya.

In terms of Asian countries, the Covid timeline of Iran displays a sharp rise of the first wave with an up-trigger of 1075 cases on March 12, 2020. A spike of 1028 infections confirmed the forecast for this wave on March 22 (Fig. 21). If this spike could have been handled, the first wave might have been averted. A steady drop in this wave was also recorded in April 2020. However, if this level of counts could have been maintained or lowered by precautionary measures, then the next up-trigger of 2705 cases on September 15, 2020, possibly could not have resulted in the next wave of infections. Here, despite early reports of the outbreak,

the government’s sluggish response due to ideology and cynicism was a major factor behind this state of the pandemic. However, make-shift treatment centers and field hospitals in stadiums, wedding halls, and parking lots across the country have been established now to respond to the rapid spread of infection [56].

A lockdown during the traditional new year holidays in April helped Myanmar suppress the infection rate despite an inferior infrastructure [57]. Still, due to poor cooperation of the local population, Myanmar saw an up-trigger of 18 cases on August 19, 2020, which, with a spike of 148 infections on September 05,

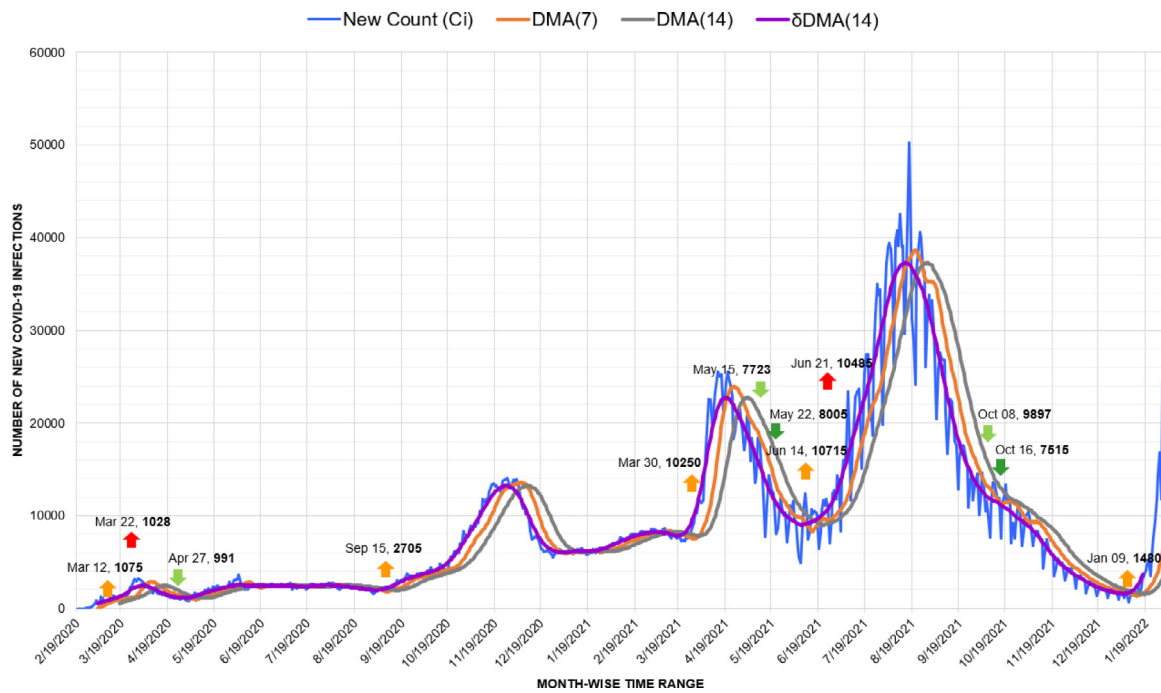


Fig. 21. Timeline graph of new Covid-19 infection cases in Iran.

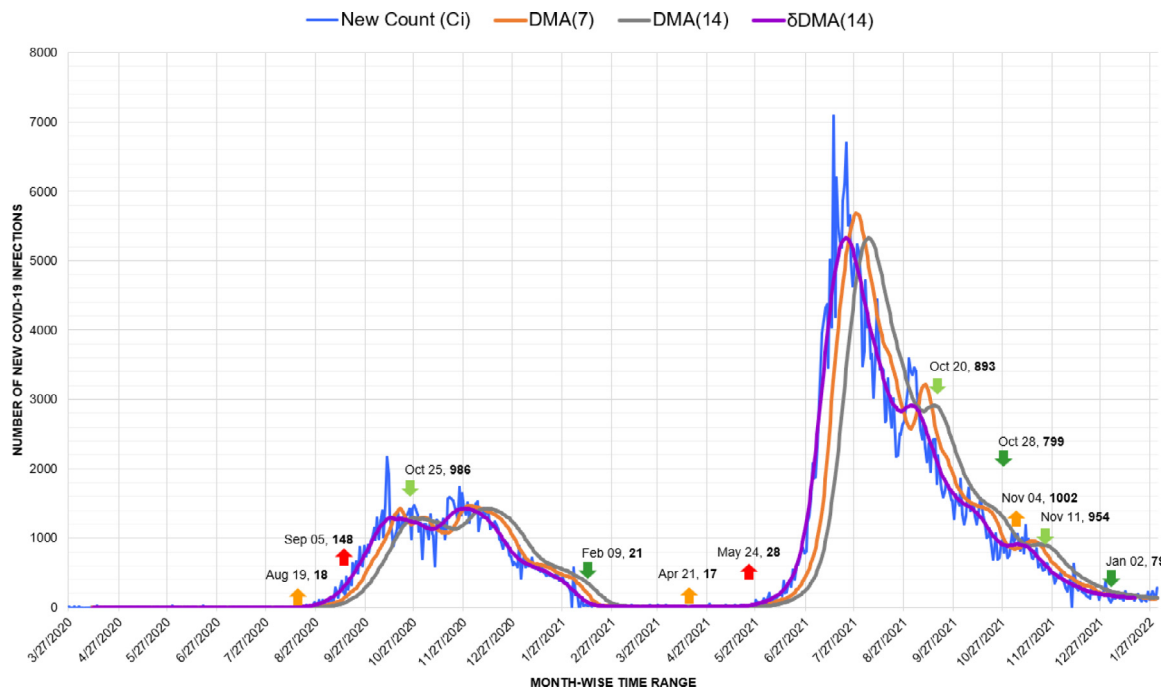


Fig. 22. Timeline graph of new Covid-19 infection cases in Myanmar.

resulted in the first wave. The spike on May 24, 2021, evolved into another sharp wave (Fig. 22). However, this wave later exhibited a steady decline to the drop marker of 799 cases on October 28, 2021. Our proposed approach effectively logged the behavior of each wave with trends and markers in the time series of Myanmar.

6.3. Observation window

As discussed in Section 5.2, the length of an observation window (w) plays a significant role in the smoothing of values by a

moving average model. It can be stated as the exact gap by which the projected values lead or lag the actual counts. Here, a larger value of w depicts a broader range of data points available for the distribution of data fluctuations by averaging. However, this large value will also increase the gap between the actual and forecasted values. Contrarily, a window (w) of a shorter gap will result in more fragmented trends and skipping of markers.

Thus, due to this reason, our proposed approach required a value of w that could project the smoothed changes in infection counts without any critical lag of time. Therefore, we selected a range of 7 to 14 days of the Covid-19 incubation period as

an observation window. For forecasting the upcoming counts, the $\chi SMA(7)$ model sums up the average of the previous 7 errors and adds it to the corresponding result of classical $SMA(7)$. This addition of errors covers the gap between projected and actual values to a much better extent compared to other baseline techniques. Elongation of w into a $\chi SMA(14)$ model will generate a forecast 7 days later compared to $\chi SMA(7)$, which may lead to missing critical changes in a wave.

Similarly, a backward displacement of DMA values by 14 units matches the trend projected by $\delta DMA(14)$ perfectly with the actual wave of infection counts. This length of displacement also makes the analysis of current trend more reliable despite short-timed spikes and drops in counts. A forecast model like $\delta DMA(7)$ with w reduced by 7 days will generate more fluctuating trends compared to $\delta DMA(14)$, leading to the skipping of critical markers in a wave. Equally, any further forward displacement higher than 14 days will place the trend far ahead in the timeline, thus impacting its credibility. Also, a longer recessive displacement will position the trend much backward compared to the actual counts rendering it useless for a forecast.

Therefore, we can deduce that the average of errors plays the same role in $\chi SMA(7)$ that the backward displacement of 14 days plays for $\delta DMA(14)$. We can also infer that any further extension of w will impact the forecast performance of models.

6.4. Implication of markers

This paper proposes 4 types of markers, namely spikes (s), drops (d), up-triggers (τ_{up}), and down-triggers (τ_{down}), for determining any significant change in the state of a Covid infection wave. As elaborated in Sections 3 and 4, these markers work on shifting the decimal base of infection counts. Here, a few points about these markers need to be elucidated.

The first question arises about the length of the observation window (w) for detecting a marker. The purpose of setting it to 7 days has been stated earlier that it is the lower limit of the incubation period advised by the WHO [42]. Within this time, the first change in infection counts can be visible at the earliest, which can help societies, governments, and medical professionals to efficiently manage and re-allocate facilities for a possible change in numbers.

The second concern arises about the placement of spikes after up-triggers and drops after down-triggers. Here, it can be observed in the timeline charts of countries that after a trigger, there may be multiple increments and decrements in the infection count. Practically, these spikes and drops are responsible for the changing behavior of a Covid-19 infection wave. However, as visible from the timelines of New Zealand and Myanmar, if the first up-trigger is properly dealt with, further spikes can be suppressed effectively for a long time.

Another question that needs attention is the logic of generating markers. As we have explained earlier, a marker is generated at the rise or fall of the decimal base of infection counts. This implies that an up-trigger of 11,449 infections was generated on April 01, 2021, in the timeline of Colombia when the numbers crossed the 10,000 mark. However, no further spikes were registered as the decimal base did not change further up to 100,000 or higher numbers. In practical terms, the wave actually continued with multiple local rises and falls until the first down-trigger of 8503 cases was visible on July 26. Generation of any marker prior to this point might have resulted in further elongation of the wave. Hence, we can conclude that the logic of decimal base shift for generating markers confirms to the nature and lethality of the pandemic. However, to further ensure the behavior of a pandemic wave, the trend values (T/D) generated by the $\delta DMA(14)$ function must also be considered. A sustained positive or negative change in these trend values is a strong indicator of wave behavior.

Table 6
Forecast precision performance of markers.

Continent	Country	Forecast precision (%)
North America	Argentina	94.594
	Colombia	93.75
Oceania	New Zealand	95.83
	Australia	84.375
South America	Cuba	90
	Jamaica	97.435
Europe	Belgium	94.594
	Croatia	98
Africa	Libya	96.428
	Kenya	95.454
Asia	Iran	94.44
	Myanmar	94.117
		94.08475

In Table 6, we have presented the forecast performance of our approach. It depicts the precision of the markers generated by the $\delta DMA(14)$ -base shift model. With the highest precision of 97.43% recorded for Jamaica and the lowest of 84.37% for Australia, our approach exhibited a fairly high average forecast performance of 94.08% for time series data of 12 countries.

6.5. Selection of MA models

We have already conferred over the forecasting limits of dedicated computational models [13–15] and ARIMA models [16,17]. Here, the attempts to forecast Covid-19 infections by making use of advanced paradigms like machine learning methods also lead to similar outcomes. This implies that, similar to previous approaches, techniques such as deep learning [58], XGboost [59], support vector machines, and regression [60] are also dependent on the generation of pre-computed forecast models. These models require massive volumes of data for computations leading to hardware restrictions, timeline concerns, and scalability issues. Moreover, life-critical data with abrupt surges in numbers like Covid-19 infection counts require a flexible and speedy computational technique that can perform swiftly over any data size. Hence, we have proposed a method capable of executing over the time series data of Covid-19 infections in a walk-forward approach. This implies that our proposed models constantly upgrade with the changes in the infection counts, leading to more sensitive and accurate forecasts about upcoming and ongoing infection waves. We dedicate this section to justify the selection of moving average models employed for specific forecasting tasks.

Earlier in Section 2.2, we elaborated that a moving average is a weighted or unweighted mean of a set of data points. We also know that several application-specific variants of moving averages are available. However, the Covid-19 data is undeniably one of the most random-natured non-stationary time series available today. The absence of any trend or seasonality in this data makes the implementation of an exponential [32,33] or weighted moving average [31,34] model enormously challenging. Hence, we are left with the option of simple unweighted moving averages.

An unweighted moving average is an estimate of the expected values of the upcoming data points in the series. It works on the property that this estimation must be approximately similar to the values falling in the range of data points consumed for generating the mean. This property enables the forecast of upcoming values in a time series according to the constantly changing numbers. $\chi SMA(7)$ employs this property to forecast the next-day count of new Covid-19 infections.

The moving average of data points also generates a 'smoothed' version of the original values. Here, smoothing implies an even distribution of any temporal fluctuation in values among the component data points during the average calculation. This 'smoothing' property of moving averages is useful for DMA models in overcoming the spikes and drops of the Covid time series data. As depicted in Fig. 8., the DMA(14) models level off all fluctuations in the time series data in a manner much better than DMA(7) models. The δ DMA(14) model further improves this smoothing by dragging it backward to match the ongoing real-time trend of infection counts.

6.6. Deployment and utilization

The framework proposed in this paper can be implemented as an independent application or a micro add-on to an existing one. The emphasis of this framework is on the nearest forecast timeline of Covid impact in a region. Hence, it can be utilized by analysts, medical authorities, and administrative bodies for estimation of the upcoming state of the Covid-19 pandemic in their region. This estimation will be vital in the timely procurement, management, and allocation of medical infrastructure and healthcare resources like medical oxygen, hospital beds, and medicines. It will also assist governing bodies in designing and implementing time-bound precautionary measures and guidelines such as sealing of borders, social distancing, and wearing masks for the population under threat.

7. Conclusion & future work

In this paper, we proposed a novel algorithmic framework to forecast the wave behavior and upcoming counts of new Covid-19 infections in a region under a minimum observation window of 7 days. We have implemented this framework on a time series database of Covid-19 infections derived from 12 countries. The framework primarily comprises a displaced double moving average (δ DMA) algorithm and a novel 'corrected moving average' (χ SMA) technique.

The framework projects the rise and fall in Covid-19 waves by detecting potential dates with specific counts called 'markers' guided by decision rules mapped through rough set theory. In combination with the positive or negative trend computed by the δ DMA(14) algorithm, these counts can be classified into triggers, spikes, and drops of an infection wave with high accuracy.

Likewise, the corrected moving average (χ SMA) algorithm computes the upcoming counts of new infections for the next day by adding the average error among the forecasted and actual counts to the upcoming forecasts. This addition of errors further corrects the forecasts, thus improving their next-day forecast precision up to 94.08%.

However, the proposed methods currently utilize predefined and constant window periods. We anticipate to improve the forecasting abilities of our framework with dynamically refreshable displacement and window periods of the component algorithms. We also intend to expand its coverage by implementing it over Covid-19 data of more countries in the future. We hope that the framework proposed in this manuscript proves itself supportive to the medical organizations and administrative authorities in allocating and managing healthcare infrastructure and medical facilities.

CRedit authorship contribution statement

Saurabh Ranjan Srivastava: Conceptualization, Data curation, Formal analysis, Investigation, Writing – original draft. **Yogesh Kumar Meena:** Conceptualization, Formal analysis, Project administration, Resources, Supervision, Validation, Review & editing. **Girdhari Singh:** Formal analysis, Resources, Supervision, Validation, Review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

Acknowledgments

The authors thank the editors and the anonymous reviewers for their helpful comments and suggestions. This work has been supported by the Science and Engineering Research Board (SERB) under the Department of Science & Technology, Government of India, for the project 'Forecasting Significant Social Events by Predictive Analytics Over Streaming Open Source Data' (Project File Number: EEQ/2019/000697).

References

- [1] B. Hu, H. Guo, P. Zhou, Z.L. Shi, Characteristics of SARS-CoV-2 and COVID-19, *Nat. Rev. Microbiol.* 19 (3) (2021) 141–154.
- [2] S. Maital, E. Barzani, The global economic impact of Covid-19: A summary of research, *Samuel Neaman Inst. Natl. Policy Res.* 2020 (2020) 1–12.
- [3] C.B. de Villiers, L. Blackburn, S. Cook, J. Janus, Sars-cov-2 variants, 2021, <https://www.finddx.org/wp-content/uploads/2021/03/COVID-variants-report-FINAL-12MAR2021.pdf>.
- [4] S.X. Zhang, F.A. Marioli, R. Gao, S. Wang, A second wave? what do people mean by covid waves? – a working definition of epidemic waves, *Risk Manag. Healthcare Policy* 14 (2021) 3775.
- [5] S.S.A. Karim, Q.A. Karim, Omicron sars-cov-2 variant: a new chapter in the Covid-19 pandemic, *Lancet* 398 (10317) (2021) 2126–2128.
- [6] S. Joshi, J. Parkar, A. Ansari, A. Vora, D. Talwar, M. Tiwaskar, S. Patil, H. Barkate, Role of favipiravir in the treatment of Covid-19, *Int. J. Infect. Dis.* 102 (2021) 501–508.
- [7] S. Felsenstein, J.A. Herbert, P.S. McNamara, C.M. Hedrich, Covid-19: Immunology and treatment options, *Clin. Immun.* 215 (2020) 108448.
- [8] A. Narin, C. Kaya, Z. Pamuk, Automatic detection of coronavirus disease (Covid-19) using x-ray images and deep convolutional neural networks, *Pattern Anal. Appl.* 24 (3) (2021) 1207–1220.
- [9] D. Pradhan, P. Biswasroy, P.K. Naik, G. Ghosh, G. Rath, A review of current interventions for Covid-19 prevention, *Arch. Med. Res.* 51 (5) (2020) 363–374.
- [10] L. Bayyurt, B. Bayyurt, Forecasting of covid-19 cases and deaths using arima models, 2020, medrxiv.
- [11] A.K. Sahai, N. Rath, V. Sood, M.P. Singh, ARIMA modelling & forecasting of Covid-19 in top five affected countries, *Diabetes Metabol. Syndrome Clin. Res. Rev.* 14 (5) (2020) 1419–1427.
- [12] M. Perc, N. Gorisek Miksic, M. Slavinec, A. Stozer, Forecasting, Covid, 19, *Front. Phys.* 8 (2020) 127.
- [13] D. Fanelli, F. Piazza, Analysis and forecast of COVID-19 spreading in China Italy and France, *Chaos Solitons Fractals* 134 (2020) 109761.
- [14] C. Anastassopoulou, L. Russo, A. Tsakris, C. Siettos, Data-based analysis, modelling and forecasting of the Covid-19 outbreak, *PLoS One* 15 (3) (2020) e0230405.
- [15] K. Sarkar, S. Khajanchi, J.J. Nieto, Modeling and forecasting the Covid-19 pandemic in India, *Chaos Solitons Fractals* 139 (2020) 110049.
- [16] A. Hernandez-Matamoros, H. Fujita, T. Hayashi, H. Perez-Meana, Forecasting of Covid-19 per regions using ARIMA models and polynomial functions, *Appl. Soft Comput.* 96 (2020) 106610.
- [17] A.C. Petrica, S. Stancu, A. Tindecu, Limitation of ARIMA models in financial and monetary economics, *Theor. Appl. Econ.* 23 (4) (2016).
- [18] R.M. Stein, Benchmarking Default Prediction Models: Pitfalls and Remedies in Model Validation, *Moody's KMV*, New York, 2002, p. 20305.
- [19] Z. Pawlak, *Rough Sets: Theoretical Aspects of Reasoning About Data*, 9, Springer Science & Business Media, 1991.
- [20] Z. Pawlak, J. Grzymala-Busse, R. Slowinski, W. Ziarko, Rough sets, *Commun. ACM* 38 (11) (1995) 88–95.
- [21] Z. Pawlak, Rough sets, *Int. J. Comput. Inf. Sci.* 11 (5) (1982) 341–356.
- [22] T. Hill, L. Marquez, M. O'Connor, W. Remus, Artificial neural network models for forecasting and decision making, *Int. J. Forecast.* 10 (1) (1994) 5–15.
- [23] Z. Pawlak, Rough sets and decision analysis, *INFOR: Inf. Syst. Oper. Res.* 38 (3) (2000) 132–144.

- [24] Y. Lu, Y. Xu, J. Huang, J. Wei, E. Herrera-Viedma, Social network clustering and consensus-based distrust behaviors management for large-scale group decision-making with incomplete hesitant fuzzy preference relations, *Appl. Soft Comput.* 117 (2022) 108373.
- [25] I. Kaliszewski, *Soft Computing for Complex Multiple Criteria Decision Making*, vol. 85, Springer Science & Business Media, 2006.
- [26] Y. Xu, M. Li, F. Chiclana, E. Herrera-Viedma, Multiplicative consistency ascertaining, inconsistency repairing, and weights derivation of hesitant multiplicative preference relations, *IEEE Trans. Syst. Man Cybern. Syst.* (2021).
- [27] R. Ihaka, *Time series analysis*, 2005.
- [28] B. Lim, S. Zohren, Time-series forecasting with deep learning: a survey, *Phil. Trans. R. Soc. A* 379 (2194) (2021) 20200209.
- [29] W. Jiang, Applications of deep learning in stock market prediction: recent progress, *Expert Syst. Appl.* 184 (2021) 115537.
- [30] U. Sahin, S. Balli, Y. Chen, Forecasting seasonal electricity generation in European countries under Covid-19-induced lockdown using fractional grey prediction models and machine learning methods, *Appl. Energy* 302 (2021) 117540.
- [31] G.E. Box, G.M. Jenkins, *Time Series Analysis: Forecasting and Control*, Holden-Day, 1976.
- [32] E.S. Gardner Jr., Exponential smoothing: The state of the art, *J. Forecast.* 4 (1) (1985) 1–28.
- [33] P.R. Winters, Forecasting sales by exponentially weighted moving average, *Manage. Sci.* 6 (3) (1960) 324–342.
- [34] A.C. Harvey, *Forecasting, Structural Time Series Models and the Kalman Filter*, Cambridge University Press, 1990.
- [35] R.J. Hyndman, *Moving Averages*, Citeseer, 2011.
- [36] N. Vandewalle, M. Ausloos, P. Boveroux, The moving averages demystified, *Phys. A* 269 (1) (1999) 170–176.
- [37] V. Alevizakos, K. Chatterjee, C. Koukouvinos, A. Lappa, A double moving average control chart: discussion, *Comm. Statist. Simulation Comput.* (2020) 1–15.
- [38] R. Mustapa, M. Latief, M. Rohandi, Double moving average method for predicting the number of patients with dengue fever in gorontalo city, in: *International Conference on Education, Science and Technology*, Redwhite Press, 2019, pp. 332–337.
- [39] Displaced moving average, 2022, <https://www.incrediblecharts.com/indicators/displacedmovingaverage.php> (Accessed 06 February 2022).
- [40] Our world in data, 2022, <https://ourworldindata.org> (Accessed 02 February 2022).
- [41] M.B. Khoo, V. Wong, A double moving average control chart, *Commun. Stat. Simul. Comput.* 37 (8) (2008) 1696–1708.
- [42] The 14-day quarantine: Understanding the coronavirus incubation period, 2022, <https://www.pfizer.com/foundations-science/14-Day-Quarantine-Incubation-Period>. (Accessed 06 February 2022).
- [43] N. Zaki, E.A. Mohamed, The estimations of the covid-19 incubation period: A scoping reviews of the literature, *J. Infect. Publ. Health* 14 (5) (2021) 638–646.
- [44] A. Stobart, S. Duckett, Australia's response to Covid-19, *Health Econ. Policy Law* 17 (1) (2022) 95–106.
- [45] U. Khair, H. Fahmi, S. Al Hakim, R. Rahim, Forecasting error calculation with mean absolute deviation and mean absolute percentage error, *J. Phys. Conf. Ser.* 930 (2017) 012002.
- [46] N.A. Gemelli, Management of COVID-19 outbreak in Argentina: the beginning, *Disaster Med. Publ. Health Preparedness* 14 (6) (2020) 815–817.
- [47] S.I. Prada, M.P. Garcia-Garcia, J. Guzman, COVID-19 response in Colombia: Hits and misses, *Health Policy Technol.* (2022) 100621.
- [48] P. Dyer, Policy and Institutional Responses to COVID-19: New Zealand, *Brookings Doha Centre*, 2021, pp. 1–25.
- [49] D. O'Sullivan, M. Rahamathulla, M. Pawar, The impact and implications of COVID-19: An Australian perspective, *Int. J. Commun. Soc. Dev.* 2 (2) (2020) 134–151.
- [50] L.L. Wylie, Cuba's response to COVID-19: lessons for the future, *J. Tourism Futures* (2021).
- [51] R. Amour, J. Robinson, I. Govia, The COVID-19 long-term care situation in jamaica, *Itccovid, Int. Long-Term Care Policy Netw.* (2020).
- [52] Y.A. Natalia, C. Faes, T. Neyens, G. Molenberghs, The COVID -19 wave in Belgium during the fall of 2020 and its association with higher education, *PLoS One* 17 (2) (2022) e0264516.
- [53] A. Sribljinic, J. Bozic, B.D. Fath, Croatian crisis management system's response to COVID -19 pandemic through the lens of a systemic resilience model, *Interdiscip. Descript. Complex Syst. INDECS* 18 (4) (2020) 408–424.
- [54] G.C. Iwendi, A.M. Alsadig, M.A. Isa, A.A. Oladunni, M.B. Musa, A. Ahmadi, Y.A. Adebisi, III. D. E. Lucero-Priso, COVID -19 in a shattered health system: Case of Libya, *J. Global Health* 11 (2021).
- [55] E.N. Wangari, P. Gichuki, A.A. Abuor, J. Wambui, S.O. Okeyo, H.T. Oyatsi, S. Odikara, B.W. Kulohoma, Kenya's response to the COVID -19 pandemic: a balance between minimizing morbidity and adverse economic impact, *AAS Open Res.* 4 (2021).
- [56] M. Ebrahimi, S.K. Gassama, K. bin Yusoff, COVID -19: Threat and response in Iran, *Iran Caucasus* 24 (4) (2020) 423–443.
- [57] M.M. Oo, N.A. Tun, X. Lin, III. D. E. Lucero-Priso, COVID -19 in myanmar: Spread actions and opportunities for peace and stability, *J. Glob. Health* 10 (2) (2020).
- [58] R. Suganya, R. Kanmani, S.G. Joyal, S. G. Advanced deep learning model for future forecasting of covid-19, *J. Phys. Conf. Ser.* 1916 (1) (2021) 012147.
- [59] L. Tahsin, S. Roy, Prediction of Covid-19 severity level using xgboost algorithm: a machine learning approach based on SIR epidemical model, *EasyChair* (2021).
- [60] H.A. Parhusip, Study on COVID-19 in the world and Indonesia using regression model of SVM bayesian ridge and gaussian, *J. Ilmiah Sains* 20 (2) (2020) 49–57.



Saurabh Ranjan Srivastava is a doctoral research scholar in the Department of Computer Science & Engineering at Malaviya National Institute of Technology Jaipur, India.

His areas of research are Data Mining & Spatiotemporal Forecasting.



Dr. Yogesh Kumar Meena is currently working as Associate Professor in the Department of Computer Science & Engineering at Malaviya National Institute of Technology Jaipur, India.

He received his Ph.D. in Computer Engineering from Malaviya National Institute of Technology Jaipur, India.

His research interests are Natural Language Processing, Information Retrieval, Data Mining and Neural Networks.



Dr. Girdhari Singh is currently working as Professor in the Department of Computer Science & Engineering at Malaviya National Institute of Technology Jaipur, India.

He received his Ph.D. in Computer Engineering from Malaviya National Institute of Technology Jaipur, India.

He is the author of textbooks on Software Engineering. His research interests are Software Engineering and Intelligent Systems.